



20010-04USA.ST25

SEQUENCE LISTING

<110> POSCO
POSTECH
An, Gynheung
Ryu, Choong-Hwan
Han, Jong-Jin
Kang, Hong-Gyu
An, Kyungsook

<120> ORGAN PREFERENTIAL GENES IDENTIFIED BY T-DNA INSERTIONAL
MUTAGENESIS OF RICE

<130> 20010-04USA

<150> 60/427,166

<151> 2002-11-15

<160> 83

<170> FastSEQ for windows Version 4.0

<210> 1

<211> 474

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (394)...(474)

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<211> 194

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<213> Oryza sativa

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<222> (104)...(194)

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<211> 325

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<213> Oryza sativa

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<220>
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 <222> (255)...(325)
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<210> 4
 <211> 650
 <212> DNA
 <213> Oryza sativa

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 <222> (560)...(650)
 <223> segment of the T-DNA insert in line 1B-207-27

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 <211> 6721
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 <213> Oryza sativa

<220>
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 <223> segment of the T-DNA insert in line 1B-138-07

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<211> 232
 <212> DNA
 <213> Oryza sativa

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<210> 7
 <211> 246
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 <213> Oryza sativa

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<212> DNA
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<223> segment of the T-DNA insert in line 1C-017-14

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<210> 9
<211> 214
<212> DNA
<213> Oryza sativa

<220>
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<222> (126)...(214)
<223> segment of the T-DNA insert in line 1C-038-56

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<210> 10
<211> 514
<212> DNA
<213> Oryza sativa

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<222> (1)...(113)
<223> segment of the T-DNA insert in line 1C-041-47

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<210> 11
<211> 603
<212> DNA

<213> *Oryza sativa*

<220>

<221> misc_feature

<222> (512)...(603)

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<210> 12

<211> 401

<212> DNA

<213> *Oryza sativa*

<220>

<221> misc_feature

<222> (1)...(96)

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<210> 13

<211> 628

<212> DNA

<213> *Oryza sativa*

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<221> misc_feature

<222> (528)...(628)

<223> segment of the T-DNA insert in line 1C-109-51

<400> 13

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tactccaaat gatgggtcat gctagcaggc ctcttcaaga taactcaggg aaatgtgtta 360
tattgtgtca tgcgcctcgc aaggaatact acaagaagtt cttttttgag gccttccctg 420
ttgagagcca tcttcaccac ttcttgcatt atcatatgaa cgctgagggtg gtggttggtg 480
tcatagaaaa caagcaagat gctgtggatt accttacttg gaccttcatt tcaaacacgg 540
atccgaggta ccaggtaacca ggtgagttcc attcttacta ccacgggtgct attttttttg 600
ctatgtggct aattacatga ctaacttg                                     628
```

<210> 14

<211> 377
 <212> DNA
 <213> Oryza sativa

<220>
 <221> misc_feature
 <222> (1)...(61)
 <223> segment of the T-DNA insert in line 1C-056-07

<400> 14
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 accagcagtg ttacttgaag gaggcggtgt ggttacctgg ttctacacac atgactccat 180
 tgcttctgca ctagtatatca tcataggctc tggagtgcct gcattttgcc taaacttctc 240
 cattttctac gtgatccatt caaccactgc agtgaccttc aatggttgctg gcaacctgaa 300
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 gaactgatca ttgcgct 377

<210> 15
 <211> 422
 <212> DNA
 <213> Oryza sativa

<220>
 <221> misc_feature
 <222> (351)...(422)
 <223> segment of the T-DNA insert in line 1C-100-32

<400> 15
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 aactcaatat gctaccact aatatctagg agttaccatt gtactaaaaa tgtataaaac 120
 atgggttgata ggagttcaga aagtgcattt atctgggtac atccgatcac tggtagaata 180
 tgttaccact tgaaccaaac tttatgtaat ttataatggg atatttgcaa ctacggaatc 240
 ttttactgct catgcaggat cacaaaggaa tttcaaattgc tgcaccagct gattgtccat 300
 tgatcccact attggtgcca aaagtagatc aatcagaagg tacagtggat accagggtgag 360
 ttccattctt actaccacgg tgctattttt tttgctatgt ggctaattac atgactaact 420
 tg 422

<210> 16
 <211> 335
 <212> DNA
 <213> Oryza sativa

<220>
 <221> misc_feature
 <222> (259)...(335)
 <223> segment of the T-DNA insert in line 1C-142-27

<400> 16
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 ttggttcgat agcaaccgct gcagttgcaa atttgcaata ttgttttagcg agtagcagcc 120
 tgcactgtcg ttgattgagg attcgttgct tgttttgcct accgtcatgg gcctttttca 180
 ggtcaccgac cgcacgagg ataagagcca agattctgta cgcgacgtcg aagcaagggc 240
 tgaggcgggt gcttgacgga ggtaccaggt gagttccatt ctactacca cggtgctatt 300
 ttttttgcta tgtggctaata tacatgacta acttg 335

<210> 17
 <211> 425
 <212> DNA
 <213> Oryza sativa

<220>
 <221> misc_feature

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<222> (332)...(425)

<223> segment of the T-DNA insert in line 1C-140-04

<400> 17

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cagatgctca tcctgctcac gctcaatgct catgctctgc tgaaatttgg cggaatttgt 120
tgcacgcatg ttgtgtttcc gtattgcatc atgtttgtat atgccaagat atgtgcttac 180
taccgtgtga gcaatgctgt tcaagaactg aatttgtttt tgcaaatgtg tcacacctgg 240
agtaggtgga aggggcagct gcagaggatg ggaggaagcc cagcatttgg gacaccttca 300
tccatcaagg tccaaaaaaa tggagtagat gacacggatc cgaggtacca ggtaccaggt 360
gagttccatt cttactacca cgggtgctatt ttttttgcta tgtggctaata tacatgacta 420
acttg
```

<210> 18

<211> 1149

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1B-115-22 - genomic DNA without T-DNA insert

<221> misc_feature

<222> (394)...(395)

<223> location in genomic DNA where T-DNA was inserted
to create line 1B-115-22

<400> 18

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aagcttaata tattaggagt agtaagctag cgtgtgagga agattcataa ccatatatca 60
tcttaattag cctttgtgat ttagcttaat cacatggcta aggcacaacc acccatccac 120
ttaactcttc attactacgc tagctacacg aggagagtag ctagctagta caggccccgg 180
caagcataaa tagcagcgtc ccctgcttcc tttcttcacg gtcctcagct catcatctgc 240
atgcagttca ctgcacacca cacagcttag ctgtctcagc ttactgacg ttcttagctg 300
cagctacttc actttgcata gtttgatcga actaaataac tcaccaagtt agctgtaatg 360
gccaaagtga tcctcgccac cttcgccgtc gtgttcatgg cgctcgccgc cacctccctc 420
gccggcgacc cggacatgct ccaggacgtc tgcgtcgccg actacaagtc cctcaaaggc 480
cgtaagtgtt ggaccattat tgttcacgca ttcataaaat atgaattgac ctattttttt 540
ttaacgaccc gtacaagaca gtgcgaagat tcatattaac gtatataatg atgtcgtgca 600
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agggcgttcc aggtcgacgg cggcatggtc gaggttcatca agtccaagtt cgtcccgcgc 1140
aaatactag
```

<210> 19

<211> 2971

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1B-164-43 - genomic DNA without T-DNA insert

<221> misc_feature

<222> (577)...(578)

<223> location in genomic DNA where T-DNA was inserted

to create line 1B-164-43

<400> 19

```

caaaaaggcg cctctaagaa ttcttcccaa acttttttgggt gttgtcaagc cgtgcgtttc 60
ggggtacatc aacggcgggc atgagctccc ggatggccgg atcggcgatc ctccgtcacg 120
tcggcgggcg cgcctcttc accgcgtcgg cgacctctcc ggcgggcgcg gcggcgggcg 180
cggcgaggcc gttccttgca ggcggagaag ccgtcccccg ggtgtggggg ttgcggctga 240
tgtccacgtc gtccgtggcg tcgacggagg cggcgggcaa ggcgagggcc aagaaggcgg 300
acgcggagaa ggagggtggg gtcaacagct actggggcat cgagcagtcg aagaagctgg 360
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```

<210> 20

<211> 4566

<212> DNA

<213> *Oryza sativa*

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1B-192-40 - genomic DNA without T-DNA insert

<221> misc_feature
 <222> (2273)...(2274)
 <223> location in genomic DNA where T-DNA was inserted
 to create line 1B-192-40

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caaactagtc atgtttcaaca ggaatgcatt gactattcga ccaagaatat ggcaccatcc 180
aacaatcaac atgggtaaaa gatgtataaa cgcctattaa tataaatgtc ctagtccact 240
ataagaatca aaagcatcta aaaactgaaa ccatattgtc caaaatacac accagcaaag 300
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gcaatagctg acgaatccga caataaccaa cggaagctc tgctctgcat caaatcacac 420
ctctcaagcc cagagggagg cgccctcacc acatggaaca atacctcgct cgacatgtgc 480
acctggcgcg gcgtgacatg ctccagcgag ctcccaaagc ctcgtttggc cgtggccttg 540
gacatggagg cacagggcct cagcggagaa atcccaccct gcatctccaa cctctcgctc 600
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```

<210> 21

<211> 1914

<212> DNA

<213> *Oryza sativa*

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1B-207-27 - genomic DNA without T-DNA insert

<221> misc_feature

<222> (906)...(907)

<223> location in genomic DNA where T-DNA was inserted
to create line 1B-207-27

<400> 21

```

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<211> 6631

<212> DNA

<213> Oryza sativa

<220>

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<223> line 1B-138-07 - genomic DNA without T-DNA insert

<221> misc_feature

<222> (1310)...(1311)

<223> location in genomic DNA where T-DNA was inserted
to create line 1B-138-07

<400> 22

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<211> 3937
<212> DNA
<213> Oryza sativa

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<221> misc_feature
<222> (0)...(0)
<223> line 1D-059-12 - genomic DNA without T-DNA insert

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<221> misc_feature
<222> (530)...(531)
<223> location in genomic DNA where T-DNA was inserted
to create line 1D-059-12

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<211> 6809

<212> DNA

<213> *Oryza sativa*

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1C-087-40 - genomic DNA without T-DNA insert

<221> misc_feature

<222> (2666)...(2667)

<223> location in genomic DNA where T-DNA was inserted
to create line 1C-087-40

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<210> 27
<211> 4284
<212> DNA
<213> Oryza sativa

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<220>
<221> misc_feature

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<222> (0)...(0)
 <223> line 1C-041-47 - genomic DNA without T-DNA insert

<221> misc_feature
 <222> (2471)...(2472)
 <223> location in genomic DNA where T-DNA was inserted
 to create line 1C-041-47

```

<400> 27
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<210> 28

<211> 3234

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1C-064-20 - genomic DNA without T-DNA insert

<221> misc_feature

<222> (2690)...(2691)

<223> location in genomic DNA where T-DNA was inserted
to create line 1C-064-20

<400> 28

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<210> 29

<211> 3677

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1C-109-35 - genomic DNA without T-DNA insert

<221> misc_feature

<222> (2301)...(2302)

<223> location in genomic DNA where T-DNA was inserted
to create line 1C-109-35

<400> 29

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ggttaatcga tcgccacctg gaccatgcat cctctctata taagctgccc tctaactagc 240
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<210> 30

<211> 8093

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1C-109-51 - genomic DNA without T-DNA insert

<221> misc_feature

<222> (6570)...(6571)

<223> location in genomic DNA where T-DNA was inserted
to create line 1C-109-51

<400> 30

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<211> 1383

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<213> Oryza sativa

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1C-056-07 - genomic DNA without T-DNA insert

<221> misc_feature

<222> (516)...(517)

<223> location in genomic DNA where T-DNA was inserted
to create line 1C-056-07

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<210> 32

<211> 7726

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1C-100-32 - genomic DNA without T-DNA insert

<221> misc_feature

<222> (5051)...(5052)

<223> location in genomic DNA where T-DNA was inserted
to create line 1C-100-32

<400> 32

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<211> 2417

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1C-142-27 - genomic DNA without T-DNA insert

<221> misc_feature

<222> (2020)...(2021)

<223> location in genomic DNA where T-DNA was inserted
to create line 1C-142-27

<400> 33

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<210> 34

<211> 4941

<212> DNA

<213> Oryza sativa

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> line 1C-140-04 - genomic DNA without T-DNA insert

<221> misc_feature
 <222> (773)...(774)
 <223> location in genomic DNA where T-DNA was inserted
 to create line 1C-140-04

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<210> 35

<211> 672

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 18-115-22 coding sequence

<400> 35

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<210> 36

<211> 999

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1B-164-43 coding sequence

<400> 36

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<210> 37

<211> 3216

<212> DNA

<213> *Oryza sativa*

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1B-192-40 coding sequence

<400> 37

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ctctcaagcc cagagggagg cgccctcacc acatggaaca atacctcgct cgacatgtgc 180
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ctcacgagaa tccacctccc caacaatggc ctctccggtg gcctcgcatc cgcagccgat 360
gttgccgggg tccgatacct caacctcagc ttcaacgcga tcggcggtgc gatcccaaaa 420
cgcttgggta cgcttcgcaa cctttcgctc ctggacttaa caaacaacaa cattcatggc 480
gagatccccg cggtgcttgg gagctcatct gccttggaat ccgtcggtct cgccgacaa 540
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tctacacttg gttcttgcgt ccggttggaa tgcgttcgtg taggaggcaa cttcctagag 1860
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aacaatttat ctggtgcaat accggatttc tttgggactt tcacctcatt acaatatcta 1980
aatatgtcat acaacaactt tgaggggcca attccagtag atggaatctt tgcggacaga 2040
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cgatgcaaac tgggaggggt ggagggtatt ctcacatgta cgataagaga aattgcatca 3180
aaattaggag ggcttagatt atctatgcta acgtga 3216

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<210> 38

<211> 1914

<212> DNA

<213> *Oryza sativa*

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1B-207-27 coding sequence

<400> 38

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ctgccacatg gcaggaagct caactggagc tctgcagccc cagtctgcac ttcattgggtt 180
ggggtgactt gcacaccaga caatagccgc gtgcaaacac tacgcctacc agcagtaggg 240
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cattccctat atcttcagca taataacctt tccgggatca taccgacttc cttacttcc 420
actttaacat ttctagatct gtcatacaac acttttgatg gagaaatccc attgagagtg 480
caaaatctca ctcaacttac tgcattgctt ctccagaata actctcttcc tggacccatc 540
cctgacctcc aactcccaaa attgaggcat ttgaatttga gcaacaataa cctcagtggt 600
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tcaccatcac ccggcaaggc caagaagggt tcttgaaaaa ggatcagaac tgggtgttata 780
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gagggaggcg ggaagttcat ccatggcaac ctaagtcac caaacatcct tctgtcacag 1440
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ccagcacgcc ttgtcggata tcgtgcacca gaagtcctcg agactaaaaa gccaaaccag 1560
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gaggatgaga	tggttcagat	gctccagggt	gcaatggcat	gtgttgccgc	ccccctgat	1800
caacggccaa	aaatggacga	ggtgatcagg	aggatcggtg	agatccggaa	ttcctactcc	1860
gggtcaagaa	caccaccgga	ggagaagcag	aaggatgaat	ctgcagcgcc	atga	1914

<210> 39

<211> 1571

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1B-138-07 coding sequence

<400> 39

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ccgcctaggg	tgcgcctcct	catcggcggg	gagttcgtcg	agtcgcgggc	cgacgagcac	120
gtcgacgtca	ccaatccggc	gacgcaggag	gtgggtgtcg	ggatcccgt	caccaccgcc	180
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gataaactgg	cagagaacat	tacaaccgaa	caggggaaga	cactgaagga	tgcttggggc	360
gatgtattcc	gtgggctagg	tggtggaaca	tgcttgtgga	atggggacac	tgcatatggg	420
tgaatatgta	tcaaatgttt	ctaacgggat	tgacaccttt	agcattaggg	agccacttgg	480
tgtatgtgct	ggaatatgtc	cattcaattt	tccagctatg	atccccctat	ggatgttccc	540
aatagcggtc	acttgtggca	atacttttgt	tctaaagcca	tcagaaaaag	atccaggggc	600
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tagatgatgc	tatccaaatt	gtgaacagaa	acaaatatgg	caatggagca	tccatatatta	1320
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tcaacgtgcc	gattccagta	cccctgccgt	tcttctcctt	caccggcagc	aaagcctcct	1440
ttgcaggaga	cttgaatttc	tacggcaagg	cgggcgtgca	gttcttcacc	cagatcaaga	1500
cggtcacgca	gcagtggaa	gagtcgccc	ctcagcgcg	ctccctctcc	atgcccacct	1560
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<210> 40

<211> 1323

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1D-059-12 coding sequence

<400> 40

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acagtcgagg	agagcgagga	tggcgtgagc	ttggcactca	tctgtctcct	ctcgcggatg	180
aagaagcacc	taggcctgga	cgcgacgtg	aagcaggaga	ccatgccgga	ggagacgggtg	240
ctcgccgttg	ctgaggtgct	gcggcggttc	tcggccctcc	gtgtcaccga	ggataagaaa	300
gttggttagat	caattgagtt	gtcgaaactg	gatgagatca	tgagcaagt	ggactctagg	360
acaattgctg	catcaccatt	tccttacaat	gtaaagctgg	aagatgttca	gtctttcttt	420

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agagagggcta agaaagaagc ttatgagaag tcacaacctt ctaagaatgg tcatgatgag 660
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gcagaaaatg gtgggggacaa agaggggtgaa actgatgatg ccaataaatc aagaacaggg 780
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gatgatccaa tttcaaggga agatttttaa gaagaatttg gcaaattcgg cacagtgcgg 960
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cataatgcac ctagaatgaa tcttaggagt gggctgaaac ttaaaataga agttgaagcc 1260
ttatggcaca caagaatgcc aacacatata tttggagtta tattatcatg gaactggcag 1320
taa 1323

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<210> 41

<211> 2568

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1C-087-40 coding sequence

<400> 41

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cggttcaacg tccccgatct ccgcgtcggc acgctcgact ccctcctcgc cctcagcgac 180
gatctcgcca agtccaacgt cttcatcgag ggggtctcgc acaagatccg gaggcagatc 240
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gtcgacacct acctcacctt tgtgtgggat gagggcaaat acccaacgat gtcaccgctc 360
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gagtatgctc tctacacggg aacattgttt gctaagggtg ttgacaactt taagggtccg 720
gcacgtgaaa aagggtttcca ggttcgcgat tttgagtata gttctgaagc acaggaaagt 780
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gaggaggacg acaccgtgct tgtgcagtcg gagtccgcca acaaggtgag ggacgacatc 2520
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<210> 42

<211> 1413

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1C-017-14 coding sequence

<400> 42

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gagtacaact acggtgactt catccccgtc ctccgcccc tctccgccc ctacctcgca 720
cgctgccacc agtcaagtc ccagcgcatg aagctcttcg aggaccactt cgtccaggaa 780
cgcagagtga tggagcagac tggtagatc cggtagcgca tggaccacat cctcgaggcc 840
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aagcggtggt tgcgccccga cgagtttagg ccggagaggt tcctggagga ggagaaggcc 1260
gtggaggcgc acggcaacga cttccgcttc gtgcccttcg gcgtcggccg ccgcagctgc 1320
cccgggatca tcctcgcgct gcccatcatc gggatcacgc tcggccgcct cgtccagagc 1380
ttcgacctgc tgccgcgcgc cgggatggac aag 1413

```

<210> 43

<211> 1227

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1C-038-56 coding sequence

<400> 43

```

gatgttcagc agcatagtgg cagtagcagc agctcaaccg aatccgacgt ccaagaaacc 60
gccgctgtcg ccgtcgccga cccctccccg cggtcggagg tcgtcgacgg cgagagcccg 120
ccgcagccgg gcggcgaggc ggcgagccat cagcagcagc agaaggagat gaagctgaag 180
aagccggaca agatcctgcc atgcccgcg tgcagcagca tggacaccaa gttctgctac 240
ttcaacaact acaacgtcaa ccagcctcgc cacttctgca agcactgcca gcgctactgg 300
accgccggcg gcgccatgcg caacgtcccc gtccggcgccg gccgccgcaa gaacaagaac 360
gccaccgccg ccgccactt cctccaccgc gtccgcgcct gcgccgccg cgccgccatg 420

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```

ccccgaggcgc cccacgacgc caccaacgcc accgtgctca gcttcggcgg cggcggaggc 480
ggacacgacg cgctgcccgt caccctggac ctgcgccaca agatgacgcg cctcggcaag 540
gaggggctcg tcgcccacgc ccggaacgcc gacgccgcgg ccgctgacag cgagggtgctg 600
agcaacaggg acgacgagca gatcggcaac actgtagcaa aacctgcaaa cgggttgacg 660
cagcatcctc ctctcctca tcatcatcat cattcagcca tgaacggtgg cggcatctgg 720
ccctactaca cctcggggat cgcgatcccg atatacccg cggcgccggc gtactggggc 780
tgcattgatt cacctcctgg agcttgaggc ctcccatggc cggccacagt ccagtctcag 840
gccatctcat catcatcacc acctacaagt gctacacctt cagtctcctc cttcacacta 900
ggcaagcatc ctagagaggg tggatgatcat gaggcaagag atcaccatgg caatggtaaa 960
gtgtgggtgc cgaagacgat ccggatcgac aacgccgacg aggttgcccg gagctcaatc 1020
cggctactct tcgccttcag aggcggcgac aaggtggacg ataacaacga cgacgatggc 1080
accagcgtgc acaagctcgc caccacgggtg ttcgagccaa agagggacgg caagacggcg 1140
aaacatccgg cgatcacgag cttgccgctc ttgcacacca accccgtcgc gcttaccgca 1200
tccgcgacct tccaggaggg atcttga

```

<210> 44
 <211> 861
 <212> DNA
 <213> Oryza sativa

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> line 1C-041-47 coding sequence

```

<400> 44
atgggcatca agggtttgac gaagcttttg gcggacaatg cgccaaggc gatgaaggag 60
cagaagtctg agagctactt cggccggcgc attgccgtcg acgccagcat gagcatctac 120
cagttcctct catttgcata ctggaagagg gaggatgcc acaaagaact aacagaggca 180
gtagaggaag gagataaaga cgcaattgaa aaattcagca agagaactgt gaaggctcacg 240
aagcagcaca atgaagaatg taaacgacta ttaagactta tgggggttcc tgttgtagag 300
gtttatgcag ttgcatcaga agatatggac tctcttactt ttggagctcc acggtttctt 360
cgctcattga tggatccaag ttccaagaaa attccagtta tggaaattga agtcgcgaaa 420
gttttgagg agcttgaact cactatggac caattcattg acttgatgat cctatctgga 480
tgtgactatt gtgatagcat taaaattgga ggtcaaacag ctctgaaact tattcgtaa 540
catgggtcca tagaaagcat tctggaaaac ataaataaag actatcagat tcctgaggac 600
tggccttatc aagaagctcg acgcttggtt aaggaaccca atgttacatt ggatattcct 660
gagctgaaat ggaatgctcc cgatgaggaa gccatagaga agattaaatt tgccaagaac 720
aaatcttccc aaggactcga atccttcttc aagccagttg ttagcacatc agtcctctg 780
aaaagaaagg acacttcaga aaaaccaacc aaagcagtcg ctaacaagaa aacaaaggga 840
gccggcgga aagaagaata a

```

<210> 45
 <211> 1653
 <212> DNA
 <213> Oryza sativa

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> line 1C-064-20 coding sequence

```

<400> 45
atggcgctcg cccccggcga cggcaagcag ggcgggcgcg gcggcgggcc ggcggtgggc 60
atcgacctcg gaacgacctt ctctgtcggt gcgggtgtggc ggcacgaccg cggcgaggtc 120
atcgccaacg accagcgcaa ccgcctcacg ccctcctgct tcgccttcac cgccgacgac 180
gacgacagct tcgtcggcga cgccgccttc aaccagtcgg cactcaaccc aaccaatacc 240
atctttgtga agcgactgat tggccgccga ttcagcgatg attctgtaca aaaagatata 300
aagctttggc ctttcaaagt cgtggcagg caagaggaca ggccgatgat cgtggtgagg 360
catgaaggcg aggaaaggca gttcatgccc gaggagatct cctccatggt gctcgccaag 420
atgagggaga cggccgagg gtacctcggc aagacggtca cgaaggccgt catcactgtc 480
ccgggtctact tcaacaacgc gcagcggcag gccaccatgg acgcccggcg catcgccggc 540
ctcaacgtga tgcgcatcat caacgagccc accgccgccc ccctcgccca ctgtctcgag 600

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```

aagatgcccc tcagcaacaa ggggaggatg gtgctcgtgt tcgatctcgg tggcggcaca 660
ttcgacatct cccttctcaa catcgatccc gaaggcaccg ccggtgacac tcaccttggc 720
ggagcggatt tcgacaacga gttggtgaag cactccttgc gagagttcaa tcggaacat 780
gggtcgtatg acattgaaag caatcagaag gcattaagga gattgaggac cgcctgcgag 840
agagcgaaga ggatgctgtc atccacgatg cagaccacca ttgaggtaga ctgctccat 900
caaggcatcg acttccgcgt caccctcacc cgatcccgat ttgaggagct gaacaaggat 960
ctcttcagca agtgcattga ggctatggag aattgcctcc gcgacgcaa ggtggacaag 1020
tggagtgttg acgatgtcgt cctcgtgggt ggctccacc gcataccaa ggtgcagaag 1080
atgctgagtg agttcttcga cggaaggag ctctgccgca gcatcaacc cgatgaagcc 1140
gtcgcgtatg gcgcccgcct ccaggcctcc attttatgtg gtggaaccga tgataagagg 1200
ttggttgata tgcttctccg cgaagtcacg ccgctctcgc taggtgttga gactgaagat 1260
aattgtacaa tgagcgtggt gatcccaagg aacactgcaa tcccgaccaa gaaggtgaaa 1320
aacttcacta ctctctacga caaccagatc aacgtgagct ttccggtgta cgaggtgag 1380
agcgaacaa ccaaggacaa caacctgctc ggcgagttca cgctatatgg catcccccg 1440
gcaccaaga gagtgccatc tatcgatgtc actttcgaca ttgatgcaa cggggtcttg 1500
aacgtttctg ccgagcacia ggtaaccgga cagaagaaca gcataccat cactaaccgc 1560
agcggacggc tgaaccagga ggaaatcgat cgcatggctc tggagcccga gaggcacaag 1620
atgaagcga tcaagcttca cgaagtagtc taa 1653

```

```

<210> 46
<211> 1437
<212> DNA
<213> Oryza sativa

```

```

<220>
<221> misc_feature
<222> (0)...(0)
<223> line 1C-109-35 coding sequence

```

```

<400> 46
atgtcgtcgt cggcgacggt ggtgccgctg gcgtaccagg ggaacacgtc ggcgctcggtg 60
gcggactggc tgaacaaggg ggacaacgcg tggcagctgg tggcggcgac gctgggtgggg 120
ctgcagagcg tgccgggctt ggtggtgctg tacggcgcg tggtgaagaa gaagtgggag 180
gtgaactcgg cgttcatggc gctctacgcc ttccgcccgg tgtggatctg ctgggtcacc 240
tgggcgtaca acatgtcgtt cgggggagaag ctctccccga tctgggggaa ggcgcgccg 300
gcgctggacc agggcctcct cgtcggccgc gcccgctgc cggcgacggt ccactaccgc 360
gccgacggga gcgtggagac ggcggcggtg gagccgctgt acccgatggc gacggtgggtg 420
tactttcagt gcgtgttcgc gcctatcacc ctcatcctcg tcgccggctc cctcctcggc 480
cgcatgagct tcctcgctg gatgatcttc gtcccgctct ggctcacctt ctctacacc 540
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tgccggcggt acgtcatcca cgtctccgcc ggcatcgccg gcttcaccgc cgcttactgg 660
gtggggcaca gggcgcagaa ggacagggag aggttcccgc cgaacaatat actgttcacg 720
ctgacggggg caggcgtgct gtggatgggg tgggcaggg tcaacggcg cggtccgtac 780
gccgccaact ccgtgcctc tatggccgtc ctcaacacca acatctgcac cgccatgagc 840
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gcggcgctgg tgatgggggt gctcggccgc agcatcccgt ggtacaccat gatgatctc 1020
cacaagcgct ccaagatcct gcagcgcgtc gacgacacc tcggcgctct ccacaccac 1080
ggcgtcggcg gcctcctcgg cggcctcctc accggcctct tcgccgagcc caccctctgc 1140
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cagttcggca agcagatcgc cggcggcctc ttctcgtcgc cctggaacgt cgtcgtcacc 1260
tcctcatct gcctcgccat caacctcctc gtcccgtcc gcatacccga cgacaagctc 1320
gaggtcggcg acgacgccgt ccacggcgag gaggcctacg cgctctgggg cgacggcgag 1380
atgtacgacg tcaccaagca cggctccgac gccgcggtt ccccgctcgt cgtatga 1437

```

```

<210> 47
<211> 6534
<212> DNA
<213> Oryza sativa

```

```

<220>
<221> misc_feature
<222> (0)...(0)

```

<223> line 1C-109-51 coding sequence

<400> 47

```

atggcggaacc tgggcggcgcg cgccgagggcg cagcgcgcgct tcaagcagta cgagtaccgc 60
gccaaactcca gcctcgtcct caccaccgac tcgcgcccccc gcgacaccca cgagcccacc 120
ggcgagccccg agacgctctg gggcaggatc gaccccagga gcttcggcga ccgcgcccgtc 180
caggccaagc cccccgagct cgaggagaag ctcaccaagt cccgcaagaa gaaggccgcc 240
gcctctgacc ccgacgacct ccaccgcccgc gacgccaagc gcaggcgccg cgccgcagcc 300
aaggagacgc aggtcagcgt cctctcgctc accgacgacg tcgtctacaa gccccagacc 360
cagccgctcg acgtcctcgg cggcgctgcc gacgaggtgc tcgccgtcct caagaatgac 480
aagatcaaga gccctgacaa gaagaaggag atcgagaagc tcctcaaccc tatctccaac 540
cagatgttctg accagatcgt ctccataggg aagctcatca cggatttcca tgatgcctcg 600
gctggtgatt cagctgctgc gccatctggt gatggcatgg acacagcgct ggatgatgac 660
atcggcggtt ctgttgaaat tgaagagaac gaagatgacg aggagagcga tttcgatcag 720
gtgcaagatg atttgatga agatgaagat gatgacttgc ctgagtcgaa tgcccctggt 780
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ttaactccga tattggagca gctacatgca acgagggcat ctgcaaagga gaggcagaag 1200
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cggttcccga agatgggcag gcaactgcac aagtgcaccc accagttacc aaagttgaat 3660
ctttcagccc atgttcagcc aattactcgt acggttttgg gttttgagtt gactataact 3720
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gaggacaacg atggcgagaa cattcttcac catgagtact tcatggttaa gaaacaatac 3840
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ccaaagccca aggaagaagg ctggtggctg gtaattgggt atagctctac caatcagttg 6360
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tgcgatcagg agtacgagtt caccgtcgat gtcattggatg ctggagggga ttga 6534<210> 48
<211> 543
<212> DNA
<213> Oryza sativa

<220>
<221> misc_feature
<222> (0)...(0)
<223> line 1C-056-07 coding sequence

<400> 48
atggttggct gccttgctac atctaccaag accatttttg cagagtctct actccacgga 60
taciaatttg acattaacac agtggtactac atggcaccct ttgccaccat gatactggct 120
ctaccagcag tgttacttga aggaggcggg gtggttacct ggttctacac acatgactcc 180
attgcttctg cactagttat catcataggg tctggaggtg ttgcattttg cctaaacttc 240

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tccatttttct acgtgatcca ttcaaccact gcagtgacct tcaatgttgc tggcaacctg 300
aaagttgtctg ttgctgtatt ggtgtcatgg ttgatcttcc ggaaccctat ctctcctatg 360
aatgcaatcg gatgcgcgat cacgctcggt gctgtactt tttatgggta tgtgaggcat 420
ttgatctctc aacagcaggc tgtagctcca ggaacaggaa gcccaacaac atcgcaaaaca 480
aattcgccga gaagtcggat ggagatgctc ccccttgtag gcgacaagca agaaaagggt 540
taa 543

```

```

<210> 49
<211> 2436
<212> DNA
<213> Oryza sativa

```

```

<220>
<221> misc_feature
<222> (0)...(0)
<223> line 1C-100-32 coding sequence

```

```

<400> 49
atggagatgg agatggagga caacaaggcg ccctcgccgc catcacctat ggagtccgac 60
gtcgtgtagg agaagcgcaa gagggaggac gatgcatcct cctccgctgt acttgccgcc 120
gccacaacaa ccggcggtgc ccagcaccac atgtggaaga ccagcctctg ctctctcttc 180
cgccgcccgc ccgcctcttc cgccgacggc tgcagccacg gcgactcctg ccgctacgcg 240
cactccgagg aggagctccg cccgcgcccc gacggcacct gggacccacac ctccgaccgc 300
gccaaagaag tccgcaaggc cgccgcccgc gaggtggagg aagagggtgt caccattgac 360
gacaaggccc tggacaagtg cctcgtcggc ctcccagggg gatgggccaac cgacaggctc 420
aagactttcc tccaagacaa ggcaagaact aactactcct ccattcttcc tcctgctcta 480
ctactaggaa tctcgtatgc aacagcgaag aagaagaagg gaatgactgt tggttttgta 540
acttttgaaa atattgaaca gctgaagaat gctatcgagg tacttacaga gaaccaatct 600
ggtggaaagg aaataaagat agcagatgcc aatcgtagat ctcatcaaaa gctgcacaca 660
gaaaagcctg tatctgacaa tggagtgaac acagaaaatg gtactagtgt tgatgttcct 720
cctggggaga catctgcacc tgaagcagca atatcaaaata aaaaaagtg cgcgatgca 780
gttactcccc ttgcccacat gtcttataat gatcagctag agcacaaaaa taattctgtt 840
gcgcagatac tgaagaggct tactcgcaat gctaggaaag cttgccctac tggcattccc 900
cttcagattt gggtttttaa atccaaagaa atttttcatt tattccattt ttcctcttta 960
gtttgtcatg attatatatt aaatcatgca ggtggctctt cttgcaagct tgaaggcatt 1020
ctggagtccc cagtgattaa tggataccgt aacaagtgtg aattctctgt gggattttct 1080
ttggagggga aaaagcgggt tggatttatg cttggaaatt ttactgatat gattgacaaa 1140
acaaaatcca gggaagggtg gactgctgtt gaggaacctg tggactgccc aaatgtctca 1200
gaaatttcct gcaaatatgc tctgatgttc caagactttc tgcagtcac aagcttgcc 1260
gtgtggaaca gagttaataa ttgtggattt tggcgtaaat tcacagttcg ggagggaga 1320
tgtcgagctc aagctgttgc acagaatgca gaaacccaaa tatcagaagt catgcttatt 1380
gttcaggttt gctccacagg tgttgatgat gcagtaatga aagatgaatt tgacaagttg 1440
accgttgccc tgcaacaagg agcagcaaca tgctcacctc cattacctt aacaactata 1500
gtagtgcaag atcacaaagg aatttcaaat gctgcaccag ctgattgtcc attgatccca 1560
ctattggtgc caaaagtaga tcaatcagaa ggtacagtgg ataaaacaag aatccatgac 1620
cacatcggtg atctgtggtt ctccatatca ccaacagcat tttttcagg caatactctc 1680
gctgcagaaa gattgtatac ccttgctggt gattgggcca acctcaattc gggcacatta 1740
ctttttgacg tatgtgtggt aacaggaaca attggactga ccttggcaca ccgtgttgaa 1800
atgggtgttg gaatcgaaat gaatgaatca gcagtttctg atgctgagag aaatgcgctc 1860
attaacgggt tatcaaattg tgcgtttgtc tgtgggaagg ccgaagatgt gatgggtct 1920
cttctcactg aatatcttgg ttcaccgcag caggacattc ctgtttctga aggtgcagta 1980
agtggtagtg tgaaagatga ggaagttatt gacagttcta agaatagtgg cgaaaatttg 2040
gacagctcaa tgcagaaaaa tgacaatggc aaaagccagc agctcgggga tgcaccagct 2100
gattcttcct cttctgccat agatgagata aaggggaatt ccaatgatag ggttggcaat 2160
gggttggaa gacagccatga tgaatacaat gaggttgctg gagaagatat tcatggggaa 2220
gcatcattga tcaatgagtc tgttgacctg aaagtatcgg actgtttgga ggacagaaag 2280
acatctgatg atggttcttc catcttaaac aatgatgtga ctgcagctac tgcagtgctag 2340
ttcgaagaca ttgttgctat tgtggatcct cctcgtgttg ggcttcccc tactgtaaac 2400
cccaaaagag gacagggagt tcctgttttc atttaa 2436

```

```

<210> 50
<211> 429
<212> DNA

```

<213> *Oryza sativa*

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1C-142-27 coding sequence

<400> 50

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atggcaatgg cttacaagat ggcgacggag gggatgaacg tgaaggagga gtgccagagg 60
tggttcatgg agatgaagtg gaagaagggtg caccggttcg tgggtgtacaa gatcgacgag 120
cggtcgcgcg ccgtgctggt ggacaagggtg ggcggccccc gcgaagggtg cgaggagctc 180
gtcgccgcgc tgcaccacga cgactgccgc tacgccgtct tcgacttcga cttcgtcacc 240
gtcgacaact gccagaagag caagatcttc ttcatcgcct caccgaccgc atcgaggata 300
agagccaaga ttctgtacgc gacgtcgaag caagggctga ggcgggtgct tgacggggtc 360
cactacgagg tgcaagccac ggactcctcc gagatgggct acgacgtcat ccgaggccgc 420
gctcagtga                                     429
```

<210> 51

<211> 1344

<212> DNA

<213> *Oryza sativa*

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1C-140-04 coding sequence

<400> 51

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atggcgaccg gagagctcgc tctcgtgtcc tcgctgttca tcgctcgtcgt gttcctcttg 60
cttggtgctg tggcgagaga ggcttctgcg ctcacccggc atgacttccc cgagggcttc 120
gtcttcggcg caggctcctc cgctttccag gtggaagggg cagctgcaga ggatgggagg 180
aagcccagca tttgggacac cttcatccat caatacatgc ctgacggctc caatgcagat 240
gtctcagcag atcagtatca ccattacaag gaggatgtaa agcttatgta tgacatgggg 300
ctggatgcgt acagattttc cattgcttgg cctcgtctta ttccgggaag aggagagatc 360
aaccccaagg gcttggagta ctacaacaat ctgatagacg aattgataat gcatatacaa 420
cctcatgtca ccatctacca ttttgatctc cctcaggccc ttcaggatga gtatggtgga 480
atactcagcc ccagattcga agattactcg gcttatgccg aggtgtgctt caagaacttc 540
ggtgacaggg tgaagcactg ggccaccttt aaccagccga acatcgagcc catcggcggc 600
ttcgacgccc gcgaccggcc gccgcggcgg tgctcctacc ccttcggcac caactgcacc 660
ggcggcgact cctcgacgga gccgtacatc gtggctcacc acctgctgct cgctcatgcc 720
tcggcagtgt ccatctacag acagaaatac cagcaggcaa ttcaaggagg ccagataggg 780
atactctca tggttcggtg gcatgagcca tacaccgaca aaacagccga tgcagctgct 840
gccattagga tgaatgaatt ccataattgga tttttgcatc ctttggtgca cggagactac 900
cctccggtga tgaggagtcg cgtgggcggg cggttgccat ccataacggc gtcagattca 960
gagaaaatac gcggatcggt cgacttcacg ggcatcaacc attactacgt tatctttgtg 1020
caatccatcg acgcgaatga gcagaaacta cgggactact acatcgacgc aggtgttcaa 1080
gaagacgaca aggagaacat tcagtgtcat tcttggctc ttggcaagggt gctgaatcac 1140
ctgaaactcg agtatggcaa cccccggtc atgatccacg aaatggtagt tattcagatt 1200
caccggatat cttcgaaaag atcaactaca acgatgactt cagatcggag ttcttgcagg 1260
gctacctgga agctctgtat ttgtccgtac ggtgcgctca ctctccttgc tacttacttc 1320
ctttgtgctg gtaaaggaag ttga                                     1344
```

<210> 52

<211> 223

<212> PRT

<213> *Oryza sativa*

<220>

<221> PEPTIDE

<222> (0)...(0)

<223> line 1B-115-22 polypeptide sequence

<400> 52

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```

Met Ala Lys Leu Ile Leu Ala Thr Phe Ala Val Val Phe Met Ala Leu
1      5      10      15
Ala Ala Thr Ser Leu Ala Gly Asp Pro Asp Met Leu Gln Asp Val Cys
20      25      30
Val Ala Asp Tyr Lys Ser Leu Lys Gly Pro Leu Arg Leu Asn Gly Phe
35      40      45
Pro Cys Lys Arg Ile Glu Asn Val Thr Ala Asn Asp Phe Phe Phe Asp
50      55      60
Gly Leu Met Lys Ala Gly Asn Thr Gly Asn Ala Val Gly Ser Val Val
65      70      75      80
Thr Ala Ala Ser Val Glu Ser Leu Pro Gly Leu Asn Thr Met Gly Val
85      90      95
Ser Met Ala Arg Ile Asp Tyr Ala Pro Trp Gly Leu Asn Pro Pro His
100     105     110
Thr His Pro Arg Ala Thr Glu Ile Ile Phe Val Val Glu Gly Ser Leu
115     120     125
Asp Val Gly Phe Val Thr Thr Ala Asn Lys Leu Phe Thr Arg Thr Val
130     135     140
Cys Lys Gly Glu Val Phe Val Phe Pro Arg Gly Leu Val His Phe Gln
145     150     155     160
Lys Asn Asn Gly Asn Thr Pro Ala Phe Ala Ile Ala Ala Leu Asn Ser
165     170     175
Gln Leu Pro Gly Thr Gln Ser Ile Ala Ala Ala Leu Phe Gly Ala Ala
180     185     190
Pro Pro Leu Pro Ser Asp Thr Leu Ala Arg Ala Phe Gln Val Asp Gly
195     200     205
Gly Met Val Glu Phe Ile Lys Ser Lys Phe Val Pro Pro Lys Tyr
210     215     220

```

<210> 53
 <211> 332
 <212> PRT
 <213> Oryza sativa

<220>
 <221> PEPTIDE
 <222> (0)...(0)
 <223> line 18-164-43 polypeptide sequence

```

<400> 53
Met Ser Ser Arg Met Ala Gly Ser Ala Ile Leu Arg His Val Gly Gly
1      5      10      15
Val Arg Leu Phe Thr Ala Ser Ala Thr Ser Pro Ala Ala Ala Ala Ala
20      25      30
Ala Ala Ala Arg Pro Phe Leu Ala Gly Gly Glu Ala Val Pro Gly Val
35      40      45
Trp Gly Leu Arg Leu Met Ser Thr Ser Ser Val Ala Ser Thr Glu Ala
50      55      60
Ala Ala Lys Ala Glu Ala Lys Lys Ala Asp Ala Glu Lys Glu Val Val
65      70      75      80
Val Asn Ser Tyr Trp Gly Ile Glu Gln Ser Lys Lys Leu Val Arg Glu
85      90      95
Asp Gly Thr Glu Trp Lys Trp Ser Cys Phe Arg Pro Trp Glu Thr Tyr
100     105     110
Thr Ala Asp Thr Ser Ile Asp Leu Thr Lys His His Val Pro Lys Thr
115     120     125
Leu Leu Asp Lys Ile Ala Tyr Trp Thr Val Lys Ser Leu Arg Phe Pro
130     135     140
Thr Asp Ile Phe Phe Gln Arg Arg Tyr Gly Cys Arg Ala Met Met Leu
145     150     155     160
Glu Thr Val Ala Ala Val Pro Gly Met Val Gly Gly Met Leu Leu His
165     170     175

```

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```

Leu Arg Ser Leu Arg Arg Phe Glu Gln Ser Gly Gly Trp Ile Arg Thr
180 185 190
Leu Leu Glu Glu Ala Glu Asn Glu Arg Met His Leu Met Thr Phe Met
195 200 205
Glu Val Ala Asn Pro Lys Trp Tyr Glu Arg Ala Leu Val Ile Thr Val
210 215 220
Gln Gly Val Phe Phe Asn Ala Tyr Phe Leu Gly Tyr Leu Leu Ser Pro
225 230 235 240
Lys Phe Ala His Arg Val Val Gly Tyr Leu Glu Glu Glu Ala Ile His
245 250 255
Ser Tyr Thr Glu Phe Leu Lys Asp Leu Glu Ala Gly Lys Ile Asp Asn
260 265 270
Val Pro Ala Pro Ala Ile Ala Ile Asp Tyr Trp Arg Leu Pro Ala Asn
275 280 285
Ala Thr Leu Lys Asp Val Val Thr Val Val Arg Ala Asp Glu Ala His
290 295 300
His Arg Asp Val Asn His Phe Ala Ser Asp Ile His Tyr Gln Gly Met
305 310 315 320
Glu Leu Lys Gln Thr Pro Ala Pro Ile Gly Tyr His
325 330

```

<210> 54

<211> 1073

<212> PRT

<213> Oryza sativa

<220>

<221> PEPTIDE

<222> (0)...(0)

<223> line 1B-192-40 polypeptide sequence

<400> 54

```

Met Val Cys Ala Ala Ile His Ile Ala Val Val Ala Met Leu Val Ser
1 5 10 15
Leu Thr Ala Leu Ala Ile Ala Asp Glu Ser Asp Asn Asn Gln Arg Glu
20 25 30
Ala Leu Leu Cys Ile Lys Ser His Leu Ser Ser Pro Glu Gly Gly Ala
35 40 45
Leu Thr Thr Trp Asn Asn Thr Ser Leu Asp Met Cys Thr Trp Arg Gly
50 55 60
Val Thr Cys Ser Ser Glu Leu Pro Lys Pro Arg Leu Val Val Ala Leu
65 70 75 80
Asp Met Glu Ala Gln Gly Leu Ser Gly Glu Ile Pro Pro Cys Ile Ser
85 90 95
Asn Leu Ser Ser Leu Thr Arg Ile His Leu Pro Asn Asn Gly Leu Ser
100 105 110
Gly Gly Leu Ala Ser Ala Ala Asp Val Ala Gly Leu Arg Tyr Leu Asn
115 120 125
Leu Ser Phe Asn Ala Ile Gly Gly Ala Ile Pro Lys Arg Leu Gly Thr
130 135 140
Leu Arg Asn Leu Ser Ser Leu Asp Leu Thr Asn Asn Asn Ile His Gly
145 150 155 160
Glu Ile Pro Pro Leu Gly Ser Ser Ser Ala Leu Glu Ser Val Gly
165 170 175
Leu Ala Asp Asn Tyr Leu Thr Gly Gly Ile Pro Leu Phe Leu Ala Asn
180 185 190
Ala Ser Ser Leu Arg Tyr Leu Ser Leu Lys Asn Asn Ser Leu Tyr Gly
195 200 205
Ser Ile Pro Ala Ala Leu Phe Asn Ser Ser Thr Ile Arg Glu Ile Tyr
210 215 220
Leu Gly Glu Asn Asn Leu Ser Gly Ala Ile Pro Pro Val Thr Ile Phe
225 230 235 240

```

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Pro Ser Gln Ile Thr Asn Leu Asp Leu Thr Thr Asn Ser Leu Thr Gly
 Gly Ile Pro Pro 245 Ser Leu Gly Asn Leu 250 Ser Ser Leu Thr Ala 255 Leu Leu
 Ala Ala Glu Asn Gln Leu Gln Gly Ser Ile Pro Asp Phe Ser Lys Leu
 Ser Ala 275 Leu Arg Tyr Leu Asp 280 Leu Ser Tyr Asn Asn 300 Leu Ser Gly Thr
 Val 290 Asn Pro Ser Val Tyr 310 Asn Met Ser Ser Ile Thr Phe Leu Gly Leu
 305 Ala Asn Asn Asn Leu Glu Gly Ile Met Pro 330 Pro Gly Ile Gly Asn Thr
 325 Leu Pro Asn Ile Gln Val Leu Ile Met Ser Asp Asn His Phe His Gly
 340 Glu Ile Pro Lys Ser Leu Ala Asn Ala Ser Asn Met Gln Phe Leu Tyr
 355 Leu Ala Asn Asn Ser Leu Arg Gly Val Ile Pro Ser Phe Gly Leu Met
 370 Thr Asp Leu Arg Val Val 390 Met Leu Tyr Ser Asn Gln Leu Glu Ala Gly
 385 Asp Trp Ala Phe Leu Ser Ser Leu Lys Asn Cys Ser Asn Leu Gln Lys
 405 Leu His Phe Gly Glu Asn Asn Leu Arg Gly Asp Met Pro Ser Ser Val
 420 Ala Glu Leu Pro Lys Thr Leu Thr Ser Leu Ala Leu Pro Ser Asn Tyr
 435 Ile Ser Gly Thr Ile Pro Leu Glu Ile Gly Asn Leu Ser Ser Ile Ser
 450 Leu Leu Tyr Leu Gly Asn Asn Leu Leu Thr Gly Ser Ile Pro His Thr
 465 Leu Gly Gln Leu Asn Asn Leu Val Val Leu Ser Leu Ser Gln Asn Ile
 485 Phe Ser Gly Glu Ile Pro Gln Ser Ile Gly Asn Leu Asn Arg Leu Thr
 500 Glu Leu Tyr Leu Ala Glu Asn Gln Leu Thr Gly Arg Ile Pro Ala Thr
 515 Leu Ser Arg Cys Gln Gln Leu Ala Leu Asn Leu Ser Cys Asn Ala
 530 Leu Thr Gly Ser Ile Ser Gly Asp Met Phe Ile Lys Leu Asn Gln Leu
 545 Ser Trp Leu Leu Asp Leu Ser His Asn Gln Phe Ile Asn Ser Ile Pro
 565 Leu Glu Leu Gly Ser Leu Ile Asn Leu Ala Ser Leu Asn Ile Ser His
 580 Asn Lys Leu Thr Gly Arg Ile Pro Ser Thr Leu Gly Ser Cys Val Arg
 595 Leu Glu Ser Leu Arg Val Gly Gly Asn Phe Leu Glu Gly Ser Ile Pro
 610 Gln Ser Leu Ala Asn Leu Arg Gly Thr Lys Val Leu Asp Phe Ser Gln
 625 Asn Asn Leu Ser Gly Ala Ile Pro Asp Phe Phe Gly Thr Phe Thr Ser
 645 Leu Gln Tyr Leu Asn Met Ser Tyr Asn Asn Phe Glu Gly Pro Ile Pro
 660 Val Asp Gly Ile Phe Ala Asp Arg Asn Lys Val Phe Val Gln Gly Asn
 675 Pro His Leu Cys Thr Asn Val Pro Met Asp Glu Leu Thr Val Cys Ser
 690 Ala Ser Ala Ser Lys Arg Lys Asn Lys Leu Ile Ile Pro Met Leu Ala
 705 Ala Phe Ser Ser Ile Ile Leu Leu Ser Ser Ile Leu Gly Leu Tyr Phe
 725 Leu Ile Val Asn Val Phe Leu Lys Arg Lys Trp Lys Ser Asn Glu His

			740					745				750				
Met	Asp	His	Thr	Tyr	Met	Glu	Leu	Lys	Thr	Leu	Thr	Tyr	Ser	Asp	Val	
		755					760					765				
Ser	Lys	Ala	Thr	Asn	Asn	Phe	Ser	Ala	Ala	Asn	Ile	Val	Gly	Ser	Gly	
	770					775					780					
His	Phe	Gly	Thr	Val	Tyr	Arg	Gly	Ile	Leu	His	Thr	Glu	Asp	Thr	Met	
	785				790					795					800	
Val	Ala	Val	Lys	Val	Phe	Lys	Leu	Asp	Gln	Cys	Gly	Ala	Leu	Asp	Ser	
				805					810					815		
Phe	Met	Ala	Glu	Cys	Lys	Ala	Leu	Lys	Asn	Ile	Arg	His	Arg	Asn	Leu	
			820					825					830			
Val	Lys	Val	Ile	Thr	Ala	Cys	Ser	Thr	Tyr	Asp	Pro	Met	Gly	Ser	Glu	
		835					840					845				
Phe	Lys	Ala	Leu	Val	Phe	Glu	Tyr	Met	Ala	Asn	Gly	Ser	Leu	Glu	Ser	
	850					855					860					
Arg	Leu	His	Thr	Lys	Phe	Asp	Arg	Cys	Gly	Asp	Leu	Ser	Leu	Gly	Glu	
	865				870					875					880	
Arg	Ile	Ser	Ile	Ala	Phe	Asp	Ile	Ala	Ser	Ala	Leu	Glu	Tyr	Leu	His	
				885					890					895		
Asn	Gln	Cys	Ile	Pro	Pro	Val	Val	His	Cys	Asp	Leu	Lys	Pro	Ser	Asn	
			900					905					910			
Val	Leu	Phe	Asn	Asn	Asp	Asp	Val	Ala	Cys	Val	Cys	Asp	Phe	Gly	Leu	
		915					920					925				
Ala	Arg	Ser	Ile	Arg	Val	Tyr	Ser	Ser	Gly	Thr	Gln	Ser	Ile	Ser	Thr	
	930					935					940					
Ser	Met	Ala	Gly	Pro	Arg	Gly	Ser	Ile	Gly	Tyr	Ile	Ala	Pro	Glu	Tyr	
	945				950					955					960	
Gly	Met	Gly	Ser	Gln	Ile	Ser	Thr	Glu	Gly	Asp	Val	Tyr	Ser	Tyr	Gly	
				965					970					975		
Ile	Ile	Leu	Leu	Glu	Met	Leu	Thr	Gly	Arg	His	Pro	Thr	Asn	Glu	Ile	
			980					985					990			
Phe	Thr	Asp	Gly	Leu	Thr	Leu	Arg	Met	Tyr	Val	Asn	Ala	Ser	Leu	Ser	
		995					1000					1005				
Gln	Ile	Lys	Asp	Ile	Leu	Asp	Pro	Arg	Leu	Ile	Pro	Glu	Met	Thr	Glu	
	1010					1015					1020					
Gln	Pro	Ser	Asn	His	Thr	Leu	Gln	Leu	His	Glu	His	Lys	Lys	Thr	Val	
	1025				1030					1035					1040	
Pro	Ser	Arg	Cys	Lys	Leu	Gly	Gly	Val	Glu	Gly	Ile	Leu	Thr	Cys	Thr	
				1045					1050					1055		
Ile	Arg	Glu	Ile	Ala	Ser	Lys	Leu	Gly	Gly	Leu	Arg	Leu	Ser	Met	Leu	
			1060					1065								

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<210> 55
<211> 637
<212> PRT
<213> Oryza sativa
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<220>  
<221> PEPTIDE  
<222> (0)...(0)  
<223> line 1B-207-27 polypeptide sequence
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<400> 55
Met Gln Asp His Ile Leu Thr Ala Phe Leu Val Val Ser Leu Leu Phe
1 5 10 15
Ala Cys Ile Pro Pro Ala Lys Ser Ala Asp Leu Asn Ser Asp Lys Gln
20 25 30
Ala Leu Leu Ala Phe Ala Ala Ser Leu Pro His Gly Arg Lys Leu Asn
35 40 45
Trp Ser Ser Ala Ala Pro Val Cys Thr Ser Trp Val Gly Val Thr Cys

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50	Thr	Pro	Asp	Asn	Ser	Arg	Val	Gln	Thr	Leu	Arg	Leu	Pro	Ala	Val	Gly
65	Leu	Phe	Gly	Pro	Leu	Pro	Ser	Asp	Thr	Leu	Gly	Lys	Leu	Asp	Ala	Leu
				85	Leu	Arg	Ser	Asn	Arg	Ile	Thr	Val	Asp	Leu	Pro	Pro
	Glu	Val	Leu	Ser	Leu	Arg	Ser	Asn	Arg	Ile	Thr	Val	Asp	Leu	Pro	Pro
				100					105					110		
	Glu	Val	Gly	Ser	Ile	Pro	Ser	Leu	His	Ser	Leu	Tyr	Leu	Gln	His	Asn
				115					120					125		
	Asn	Leu	Ser	Gly	Ile	Ile	Pro	Thr	Ser	Leu	Thr	Ser	Thr	Leu	Thr	Phe
				130					135					140		
	Leu	Asp	Leu	Ser	Tyr	Asn	Thr	Phe	Asp	Gly	Glu	Ile	Pro	Leu	Arg	Val
																160
	Gln	Asn	Leu	Thr	Gln	Leu	Thr	Ala	Leu	Leu	Gln	Asn	Asn	Ser	Leu	Leu
					165					170					175	
	Ser	Gly	Pro	Ile	Pro	Asp	Leu	Gln	Leu	Pro	Lys	Leu	Arg	His	Leu	Asn
				180						185				190		
	Leu	Ser	Asn	Asn	Asn	Leu	Ser	Gly	Pro	Ile	Pro	Pro	Ser	Leu	Gln	Arg
				195					200					205		
	Phe	Pro	Ala	Asn	Ser	Phe	Leu	Gly	Asn	Ala	Phe	Leu	Cys	Gly	Phe	Pro
							215					220				
	Leu	Gln	Pro	Cys	Pro	Gly	Thr	Ala	Pro	Ser	Pro	Ser	Pro	Ser	Pro	Thr
							230					235				240
	Ser	Pro	Ser	Pro	Gly	Lys	Ala	Lys	Lys	Gly	Phe	Trp	Lys	Arg	Ile	Arg
					245										255	
	Thr	Gly	Val	Ile	Ala	Leu	Ala	Ala	Ala	Gly	Gly	Val	Leu	Leu	Leu	Leu
				260					265					270		
	Ile	Leu	Ile	Val	Leu	Leu	Leu	Ile	Cys	Ile	Phe	Lys	Arg	Lys	Lys	Ser
				275					280					285		
	Thr	Glu	Pro	Thr	Thr	Ala	Ser	Ser	Ser	Lys	Gly	Lys	Thr	Val	Ala	Gly
							295						300			
	Gly	Arg	Gly	Glu	Asn	Pro	Lys	Glu	Glu	Tyr	Ser	Ser	Gly	Val	Gln	Glu
						310					315					320
	Ala	Glu	Arg	Asn	Lys	Leu	Val	Phe	Phe	Glu	Gly	Cys	Ser	Tyr	Asn	Phe
					325					330					335	
	Asp	Leu	Glu	Asp	Leu	Leu	Arg	Ala	Ser	Ala	Glu	Val	Leu	Gly	Lys	Gly
					340					345				350		
	Ser	Tyr	Gly	Thr	Thr	Tyr	Lys	Ala	Val	Leu	Glu	Asp	Gly	Thr	Thr	Val
								360					365			
	Val	Val	Lys	Arg	Leu	Lys	Glu	Val	Val	Val	Gly	Lys	Lys	Asp	Phe	Glu
							375						380			
	Gln	Gln	Met	Glu	Ile	Val	Gly	Arg	Val	Gly	Gln	His	Gln	Asn	Val	Val
						390					395					400
	Pro	Leu	Arg	Ala	Tyr	Tyr	Tyr	Ser	Lys	Asp	Glu	Lys	Leu	Leu	Val	Tyr
					405					410					415	
	Asp	Tyr	Ile	Pro	Ser	Gly	Ser	Leu	Ala	Val	Val	Leu	His	Gly	Asn	Lys
					420				425					430		
	Ala	Thr	Gly	Lys	Ala	Pro	Leu	Asp	Trp	Glu	Thr	Arg	Val	Lys	Ile	Ser
								440					445			
	Leu	Gly	Val	Ala	Arg	Gly	Ile	Ala	His	Leu	His	Ala	Glu	Gly	Gly	Gly
							455						460			
	Lys	Phe	Ile	His	Gly	Asn	Leu	Lys	Ser	Ser	Asn	Ile	Leu	Leu	Ser	Gln
						470					475					480
	Asn	Leu	Asp	Gly	Cys	Val	Ser	Glu	Phe	Gly	Leu	Ala	Gln	Leu	Met	Thr
					485					490					495	
	Ile	Pro	Pro	Ala	Pro	Ala	Arg	Leu	Val	Gly	Tyr	Arg	Ala	Pro	Glu	Val
					500				505					510		
	Leu	Glu	Thr	Lys	Lys	Pro	Thr	Gln	Lys	Ser	Asp	Val	Tyr	Ser	Phe	Gly
								520					525			
	Val	Leu	Val	Leu	Glu	Met	Leu	Thr	Gly	Lys	Ala	Pro	Leu	Arg	Ser	Pro
							535					540				
	Gly	Arg	Glu	Asp	Ser	Ile	Glu	His	Leu	Pro	Arg	Trp	Val	Gln	Ser	Val
						550					555					560

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Val	Arg	Glu	Glu	Trp	Thr	Ala	Glu	Val	Phe	Asp	Val	Asp	Leu	Leu	Arg
				565					570					575	
His	Pro	Asn	Ile	Glu	Asp	Glu	Met	Val	Gln	Met	Leu	Gln	Val	Ala	Met
			580					585					590		
Ala	Cys	Val	Ala	Ala	Pro	Pro	Asp	Gln	Arg	Pro	Lys	Met	Asp	Glu	Val
		595					600					605			
Ile	Arg	Arg	Ile	Val	Glu	Ile	Arg	Asn	Ser	Tyr	Ser	Gly	Ser	Arg	Thr
	610					615					620				
Pro	Pro	Glu	Glu	Lys	Gln	Lys	Asp	Glu	Ser	Ala	Ala	Pro			
625					630					635					

<210> 56
 <211> 523
 <212> PRT
 <213> Oryza sativa

<220>
 <221> PEPTIDE
 <222> (0)...(0)
 <223> line 1B-138-07 polypeptide sequence

<400> 56

Met	Ala	Ala	Pro	Leu	Ser	Thr	Ala	Ala	Ala	Ala	Ser	Trp	Leu	Ser	Asp
1				5					10					15	
Ser	Ala	Ser	Ser	Pro	Pro	Arg	Val	Arg	Leu	Leu	Ile	Gly	Gly	Glu	Phe
			20					25					30		
Val	Glu	Ser	Arg	Ala	Asp	Glu	His	Val	Asp	Val	Thr	Asn	Pro	Ala	Thr
		35					40					45			
Gln	Glu	Val	Val	Ser	Arg	Ile	Pro	Leu	Thr	Thr	Ala	Asp	Glu	Phe	Arg
	50					55					60				
Ala	Ala	Val	Asp	Ala	Ala	Arg	Thr	Ala	Phe	Pro	Gly	Trp	Arg	Asn	Thr
65				70					75					80	
Pro	Val	Thr	Thr	Arg	Gln	Arg	Ile	Met	Leu	Lys	Tyr	Gln	Glu	Leu	Ile
				85				90					95		
Arg	Ala	Asn	Met	Asp	Lys	Leu	Ala	Glu	Asn	Ile	Thr	Thr	Glu	Gln	Gly
			100					105					110		
Lys	Thr	Leu	Lys	Asp	Ala	Trp	Gly	Asp	Val	Phe	Arg	Gly	Leu	Glu	Val
		115					120					125			
Val	Glu	His	Ala	Cys	Gly	Met	Gly	Thr	Leu	Gln	Met	Gly	Glu	Tyr	Val
	130				135						140				
Ser	Asn	Val	Ser	Asn	Gly	Ile	Asp	Thr	Phe	Ser	Ile	Arg	Glu	Pro	Leu
145					150				155					160	
Gly	Val	Cys	Ala	Gly	Ile	Cys	Pro	Phe	Asn	Phe	Pro	Ala	Met	Ile	Pro
			165					170					175		
Leu	Trp	Met	Phe	Pro	Ile	Ala	Val	Thr	Cys	Gly	Asn	Thr	Phe	Val	Leu
		180						185					190		
Lys	Pro	Ser	Glu	Lys	Asp	Pro	Gly	Ala	Ala	Met	Met	Leu	Ala	Glu	Leu
		195					200					205			
Ala	Met	Glu	Ala	Gly	Leu	Pro	Lys	Gly	Val	Leu	Asn	Ile	Val	His	Gly
	210					215					220				
Thr	His	Asp	Val	Val	Asn	Asn	Ile	Cys	Asp	Asp	Glu	Asp	Ile	Lys	Ala
225					230				235					240	
Val	Ser	Phe	Val	Gly	Ser	Asn	Ile	Ala	Gly	Met	His	Ile	Tyr	Ser	Arg
			245						250					255	
Ala	Ser	Ala	Lys	Gly	Lys	Arg	Val	Gln	Ser	Asn	Met	Gly	Ala	Lys	Asn
			260					265					270		
His	Ala	Ile	Ile	Leu	Pro	Asp	Ala	Asp	Arg	Asp	Ala	Thr	Leu	Asn	Ala
		275					280					285			
Leu	Ile	Ala	Ala	Gly	Phe	Gly	Ala	Ala	Gly	Gln	Arg	Cys	Met	Ala	Leu
	290					295					300				
Ser	Thr	Ala	Val	Phe	Val	Gly	Gly	Ser	Glu	Pro	Trp	Ile	Arg	Pro	Gly
305					310					315					320

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Ile Arg Glu Asp Glu Leu Val Lys Arg Ala Ser Ser Leu Val Val Asn
          325          330
Ser Gly Met Ala Ser Asp Ala Asp Leu Gly Pro Val Ile Ser Lys Gln
          340          345          350
Ala Lys Glu Arg Ile Cys Lys Leu Ile Gln Ser Gly Ala Asp Asn Gly
          355          360          365
Ala Arg Val Leu Leu Asp Gly Arg Asp Ile Val Val Pro Asn Phe Glu
          370          375          380
Asn Gly Asn Phe Val Gly Pro Thr Leu Leu Ala Asp Val Lys Ser Glu
          385          390          395          400
Met Glu Cys Tyr Lys Glu Glu Ile Phe Gly Pro Val Leu Leu Leu Met
          405          410          415
Lys Ala Glu Ser Leu Asp Asp Ala Ile Gln Ile Val Asn Arg Asn Lys
          420          425          430
Tyr Gly Asn Gly Ala Ser Ile Phe Thr Thr Ser Gly Val Ser Ala Arg
          435          440          445
Lys Phe Gln Thr Asp Ile Glu Ala Gly Gln Val Gly Ile Asn Val Pro
          450          455          460
Ile Pro Val Pro Leu Pro Phe Phe Ser Phe Thr Gly Ser Lys Ala Ser
          465          470          475          480
Phe Ala Gly Asp Leu Asn Phe Tyr Gly Lys Ala Gly Val Gln Phe Phe
          485          490          495
Thr Gln Ile Lys Thr Val Thr Gln Gln Trp Lys Glu Ser Pro Ala Gln
          500          505          510
Arg Val Ser Leu Ser Met Pro Thr Ser Gln Lys
          515          520

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<210> 57

<211> 446

<212> PRT

<213> Oryza sativa

<220>

<221> PEPTIDE

<222> (0)...(0)

<223> line 1D-059-12 polypeptide sequence

<400> 57

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  1      5      10
Lys Glu Val Leu Arg Gln Val Glu Phe Tyr Phe Ser Asp Ser Asn Leu
      20      25      30
Pro Arg Asp Asn Phe Leu Arg Lys Thr Val Glu Glu Ser Glu Asp Gly
      35      40      45
Leu Val Ser Leu Ala Leu Ile Cys Ser Phe Ser Arg Met Lys Lys His
      50      55      60
Leu Gly Leu Asp Ala Asp Val Lys Gln Glu Thr Met Pro Glu Glu Thr
      65      70      75      80
Val Leu Ala Val Ala Glu Val Leu Arg Arg Ser Ser Ala Leu Arg Val
      85      90      95
Thr Glu Asp Gly Lys Lys Val Gly Arg Ser Ile Glu Leu Ser Lys Leu
      100      105      110
Asp Glu Ile Met Glu Gln Val Asp Ser Arg Thr Ile Ala Ala Ser Pro
      115      120      125
Phe Pro Tyr Asn Val Lys Leu Glu Asp Val Gln Ser Phe Phe Ala Gln
      130      135      140
Tyr Gly Lys Val Asn Ser Val Arg Leu Pro Arg His Ile Ala Asp Lys
      145      150      155      160
Arg His Phe Cys Gly Thr Ala Leu Val Glu Phe Ser Glu Glu Glu Glu
      165      170      175
Ala Asn Ala Val Leu Lys Asn Thr Leu Val Phe Ala Gly Ala Asp Leu
      180      185      190

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Glu Ile Lys Pro Lys Lys Glu Phe Asp Thr Glu Arg Glu Ala Lys Lys
 195 200 205
 Glu Ala Tyr Glu Lys Ser Gln Pro Thr Lys Asn Gly His Asp Glu Gly
 210 215 220
 Tyr Pro Lys Gly Leu Ile Val Ala Phe Lys Leu Lys Ile Ile Gln Ile
 225 230 235 240
 Asp Gly Gly Met Ala Glu Asn Gly Gly Asp Lys Glu Gly Glu Thr Asp
 245 250 255
 Asp Ala Asn Lys Ser Arg Thr Gly His Asp Glu Lys Ile Pro Glu Asn
 260 265 270
 Ser Asp Ile Lys Glu Asp Leu Ser Asp Asp Val Glu Lys Ser Lys Glu
 275 280 285
 Ala Ala Ala Gln Ser Val Lys Lys Gly Glu Ser Pro Ser Glu Asn Ala
 290 295 300
 Asp Asp Pro Ile Ser Arg Glu Asp Phe Lys Glu Glu Phe Gly Lys Phe
 305 310 315 320
 Gly Thr Val Arg Tyr Val Asp Phe Ser Ile Gly Glu Asp Ser Gly Tyr
 325 330 335
 Ile Arg Phe Glu Asp Ser Lys Ala Ala Glu Lys Ala Arg Ala Leu Ala
 340 345 350
 Ala Ile Ser Asp Glu Gly Gly Leu Ile Met Lys Gly His Leu Val Thr
 355 360 365
 Leu Glu Pro Val Ser Gly Gln Ala Glu Lys Asp Tyr Trp Ser Ala Ile
 370 375 380
 Lys Gly Gly Gln Gly Lys Tyr Arg Asp Asn Arg Ser Asn Arg Gly Arg
 385 390 395 400
 Ala Asp Pro Leu Lys Tyr His Asn Ala Pro Arg Met Asn Leu Arg Ser
 405 410 415
 Gly Leu Lys Leu Lys Ile Glu Val Glu Ala Leu Trp His Thr Arg Met
 420 425 430
 Pro Thr His Ile Phe Gly Val Ile Leu Ser Trp Asn Trp Gln
 435 440 445

<210> 58

<211> 859

<212> PRT

<213> Oryza sativa

<220>

<221> PEPTIDE

<222> (0)...(0)

<223> line 1C-087-40 polypeptide sequence

<400> 58

Met Ala Thr Arg Tyr Trp Ile Val Ser Leu Pro Val Gln Thr Pro Gly
 1 5 10 15
 Ser Thr Ala Asn Ser Leu Trp Ala Arg Leu Gln Asp Ser Ile Ser Arg
 20 25 30
 His Ser Phe Asp Thr Pro Leu Tyr Arg Phe Asn Val Pro Asp Leu Arg
 35 40 45
 Val Gly Thr Leu Asp Ser Leu Leu Ala Leu Ser Asp Asp Leu Val Lys
 50 55 60
 Ser Asn Val Phe Ile Glu Gly Val Ser His Lys Ile Arg Arg Gln Ile
 65 70 75 80
 Glu Glu Leu Glu Arg Ala Gly Gly Val Glu Ser Gly Ala Leu Thr Val
 85 90 95
 Asp Gly Val Pro Val Asp Thr Tyr Leu Thr Arg Phe Val Trp Asp Glu
 100 105 110
 Gly Lys Tyr Pro Thr Met Ser Pro Lys Glu Ile Val Gly Ser Ile
 115 120 125
 Gln Ser Gln Val Ser Lys Ile Glu Asp Asp Met Lys Val Arg Gly Ala
 130 135 140

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Glu	Tyr	Asn	Asn	Val	Arg	Ser	Gln	Leu	Ser	Ala	Ile	Asn	Arg	Lys	Gln
145					150					155					160
Thr	Gly	Ser	Leu	Ala	Val	Arg	Asp	Leu	Ser	Asn	Leu	Val	Lys	Pro	Glu
				165					170					175	
Asp	Met	Val	Thr	Ser	Glu	His	Leu	Val	Thr	Leu	Leu	Ala	Val	Val	Pro
			180					185					190		
Lys	Tyr	Ser	Gln	Lys	Asp	Trp	Leu	Ser	Ser	Tyr	Glu	Ser	Leu	Asp	Thr
		195					200					205			
Phe	Val	Val	Pro	Arg	Ser	Ser	Lys	Lys	Leu	Tyr	Glu	Asp	Asn	Glu	Tyr
	210					215					220				
Ala	Leu	Tyr	Thr	Val	Thr	Leu	Phe	Ala	Lys	Val	Val	Asp	Asn	Phe	Lys
225					230					235					240
Val	Arg	Ala	Arg	Glu	Lys	Gly	Phe	Gln	Val	Arg	Asp	Phe	Glu	Tyr	Ser
				245					250					255	
Ser	Glu	Ala	Gln	Glu	Ser	Arg	Lys	Glu	Glu	Leu	Glu	Lys	Leu	Met	Gln
			260					265					270		
Asp	Gln	Glu	Ala	Met	Arg	Ala	Ser	Leu	Leu	Gln	Trp	Cys	Tyr	Ala	Ser
		275					280					285			
Tyr	Ser	Glu	Asn	Thr	Ile	Tyr	Val	Arg	His	Ala	Lys	Val	Gln	Asn	Phe
	290					295					300				
Val	Leu	Leu	Tyr	Val	Phe	Ser	Ser	Trp	Met	His	Phe	Cys	Ala	Val	Arg
305					310					315					320
Val	Phe	Val	Glu	Ser	Ile	Leu	Arg	Tyr	Gly	Leu	Pro	Pro	Ser	Phe	Leu
				325					330					335	
Ser	Ala	Val	Leu	Ala	Pro	Ser	Gln	Lys	Gly	Glu	Lys	Lys	Val	Arg	Ser
			340					345					350		
Ile	Leu	Glu	Glu	Leu	Cys	Gly	Asn	Val	His	Ser	Ile	Tyr	Trp	Lys	Ser
		355					360					365			
Glu	Asp	Asp	Val	Gly	Val	Ala	Gly	Leu	Gly	Glu	His	Arg	Val	Arg	Cys
	370					375					380				
Cys	Gly	Tyr	Tyr	Val	Phe	Val	Thr	Leu	Ser	Ser	Gln	Lys	Asp	Lys	Leu
385					390					395					400
Gly	Val	Met	Tyr	Arg	Thr	Ser	Ile	Leu	Gly	Asp	Pro	Val	Pro	Thr	Asp
				405					410					415	
Asp	Ser	Arg	Val	Asp	Lys	Thr	Gln	Glu	Glu	Met	Met	Val	Lys	Glu	Lys
			420					425					430		
Glu	Ile	His	Val	Met	Ser	Asn	Arg	Arg	Lys	Arg	Gly	Glu	Ser	Lys	
		435					440				445				
Pro	Gln	Ala	His	Asp	Ala	Gly	Asp	Thr	Thr	Pro	Ile	Asp	Asn	Ile	Leu
	450					455					460				
Thr	Ser	Leu	Asp	Asp	Ala	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Arg	Arg	Glu
465					470					475					480
Leu	Pro	Leu	Leu	Gln	Leu	Asn	Asp	His	Gln	Glu	Ala	Asp	Asp	Ala	Asp
				485					490					495	
Ala	Ser	Ser	Ser	Ser	Ser	Pro	His	Gln	Gln	Arg	Arg	Leu	Trp	Val	Lys
				500				505					510		
Asp	Arg	Ser	Arg	Ala	Trp	Trp	Glu	Leu	Cys	Ser	Ser	Ala	Asp	Tyr	Pro
		515					520					525			
Glu	Ala	Asp	Phe	Arg	Arg	Ala	Phe	Arg	Met	Ser	Arg	Pro	Thr	Phe	His
	530					535					540				
Phe	Leu	Cys	Asp	Ala	Leu	Ala	Ala	Ala	Val	Ala	Lys	Glu	Asp	Thr	Ala
545					550					555					560
Leu	Arg	Ala	Ala	Ile	Pro	Val	Arg	Gln	Arg	Val	Ala	Val	Cys	Val	Trp
				565					570					575	
Arg	Leu	Ala	Thr	Gly	Glu	Pro	Leu	Arg	Val	Val	Ser	Lys	Arg	Phe	Gly
			580					585					590		
Leu	Gly	Ile	Ser	Thr	Cys	His	Lys	Leu	Ile	Leu	Glu	Val	Cys	Ala	Ala
		595					600					605			
Ile	Arg	Asn	Leu	Leu	Met	Pro	Arg	Phe	Leu	His	Trp	Pro	Asp	His	Pro
	610					615					620				
Thr	Ser	Thr	Ala	Tyr	Lys	Thr	Arg	Phe	Glu	Ala	Thr	Ser	Gly	Val	Ser
625					630					635					640
Gly	Val	Val	Gly	Ala	Met	Tyr	Thr	Thr	His	Ile	Pro	Ile	Ile	Ala	Pro

Lys	Val	Ser	Val	Ala	Ala	Tyr	Leu	Asn	Arg	Arg	His	Thr	Glu	Arg	Asn
His	Lys	Thr	Ser	Tyr	Ser	Ile	Thr	Leu	Gln	Gly	Val	Val	Gly	Pro	Asp
Gly	Thr	Phe	Thr	Asp	Val	Cys	Ile	Gly	Trp	Pro	Gly	Ser	Met	Ser	Asp
Glu	Gln	Val	Leu	Arg	Lys	Ser	Ala	Leu	His	Gln	Arg	Ala	Ser	Ala	Ala
Ala	Gly	Ser	Met	Ser	Trp	Val	Val	Gly	Gly	Ala	Ser	Tyr	Pro	Leu	Thr
Glu	Trp	Met	Leu	Val	Pro	Tyr	Ala	Gln	Arg	Asn	Leu	Thr	Trp	Thr	Gln
His	Ala	Phe	Asn	Glu	Lys	Val	Gly	Glu	Val	Arg	Arg	Val	Ala	Thr	Glu
Ala	Phe	Val	Arg	Leu	Lys	Gly	Arg	Trp	Ala	Cys	Leu	Gln	Lys	Arg	Thr
Glu	Val	Lys	Leu	Gln	Asp	Leu	Pro	Ala	Val	Leu	Ala	Ala	Cys	Cys	Val
Leu	His	Asn	Ile	Cys	Glu	Thr	Arg	Gly	Glu	Asp	Met	Asp	Pro	Asp	Leu
Arg	Cys	Asp	Leu	Pro	Pro	Asp	Glu	Glu	Glu	Asp	Asp	Thr	Val	Leu	Val
Gln	Ser	Glu	Ser	Ala	Asn	Lys	Val	Arg	Asp	Asp	Ile	Ala	His	Asn	Leu
Leu	His	Arg	Gly	Leu	Ala	Gly	Thr	Ala	Phe	Phe					

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<210> 59
<211> 473
<212> PRT
<213> Oryza sativa
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<220>  
<221> PEPTIDE  
<222> (0)...(0)  
<223> line 1C-017-14 polypeptide sequence
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<400>	59														
Met	Asp	Ala	Leu	Leu	Val	Glu	Lys	Val	Leu	Leu	Gly	Leu	Phe	Val	Ala
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Ala	Val	Leu	Ala	Leu	Val	Val	Ala	Lys	Leu	Thr	Gly	Lys	Arg	Leu	Arg
			20					25					30		
Leu	Pro	Pro	Gly	Pro	Ala	Gly	Ala	Pro	Ile	Val	Gly	Asn	Trp	Leu	Gln
		35					40					45			
Val	Gly	Asp	Asp	Leu	Asn	His	Arg	Asn	Leu	Met	Ala	Leu	Ala	Arg	Arg
	50					55					60				
Phe	Gly	Asp	Ile	Leu	Leu	Leu	Arg	Met	Gly	Val	Arg	Asn	Leu	Val	Val
65				70						75					80
Val	Ser	Ser	Pro	Asp	Leu	Ala	Lys	Glu	Val	Leu	His	Thr	Gln	Gly	Val
				85					90					95	
Glu	Phe	Gly	Ser	Arg	Thr	Arg	Asn	Val	Val	Phe	Asp	Ile	Phe	Thr	Gly
			100					105					110		
Lys	Gly	Gln	Asp	Met	Val	Phe	Thr	Val	Tyr	Gly	Asp	His	Trp	Arg	Lys
		115					120					125			
Met	Arg	Arg	Ile	Met	Thr	Val	Pro	Phe	Phe	Thr	Asn	Lys	Val	Val	Ala
	130					135					140				
Gln	Asn	Arg	Ala	Gly	Trp	Glu	Glu	Glu	Ala	Arg	Leu	Val	Val	Glu	Asp
145					150					155					160
Val	Arg	Arg	Asp	Pro	Thr	Ala	Ala	Thr	Ser	Gly	Val	Val	Ile	Arg	Arg
				165					170					175	
Arg	Leu	Gln	Leu	Met	Met	Tyr	Asn	Asp	Met	Phe	Arg	Ile	Met	Phe	Asp

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Arg	Arg	Phe	180	Asp	Ser	Val	Asp	Asp	185	Pro	Leu	Phe	Asn	Lys	190	Leu	Lys	Ala
		195						200						205				
Phe	Asn	Ala	Glu	Arg	Ser	Arg	215	Leu	Ser	Gln	Ser	Phe	Glu	Tyr	Asn	Tyr		
	210											220						
Gly	Asp	Phe	Ile	Pro	Val	Leu	Arg	Pro	Phe	Leu	Arg	Arg	Tyr	Leu	Ala			
	225				230					235					240			
Arg	Cys	His	Gln	Leu	Lys	Ser	Gln	Arg	Met	Lys	Leu	Phe	Glu	Asp	His			
			245						250					255				
Phe	Val	Gln	Glu	Arg	Lys	Arg	Val	Met	Glu	Gln	Thr	Gly	Glu	Ile	Arg			
		260						265						270				
Cys	Ala	Met	Asp	His	Ile	Leu	Glu	Ala	Glu	Arg	Lys	Gly	Glu	Ile	Asn			
	275						280					285						
His	Asp	Asn	Val	Leu	Tyr	Ile	Val	Glu	Asn	Ile	Asn	Val	Ala	Ala	Ile			
	290					295					300							
Glu	Thr	Thr	Leu	Trp	Ser	Ile	Glu	Trp	Gly	Ile	Ala	Glu	Leu	Val	Asn			
	305				310					315					320			
His	Pro	Ser	Ile	Gln	Ser	Lys	Val	Arg	Glu	Glu	Met	Ala	Ser	Val	Leu			
			325						330					335				
Gly	Gly	Ala	Ala	Val	Thr	Glu	Pro	Asp	Leu	Glu	Arg	Leu	Pro	Tyr	Leu			
		340						345					350					
Gln	Ala	Val	Val	Lys	Glu	Thr	Leu	Arg	Leu	Arg	Met	Ala	Ile	Pro	Leu			
	355						360					365						
Leu	Val	Pro	His	Met	Asn	Leu	Ala	Asp	Gly	Lys	Leu	Ala	Gly	Tyr	Asp			
	370				375						380							
Ile	Pro	Ala	Glu	Ser	Lys	Ile	Leu	Val	Asn	Ala	Trp	Phe	Leu	Ala	Asn			
	385				390				395						400			
Asp	Pro	Lys	Arg	Trp	Val	Arg	Pro	Asp	Glu	Phe	Arg	Pro	Glu	Arg	Phe			
			405						410					415				
Leu	Glu	Glu	Glu	Lys	Ala	Val	Glu	Ala	His	Gly	Asn	Asp	Phe	Arg	Phe			
		420						425					430					
Val	Pro	Phe	Gly	Val	Gly	Arg	Arg	Ser	Cys	Pro	Gly	Ile	Ile	Leu	Ala			
	435					440					445							
Leu	Pro	Ile	Ile	Gly	Ile	Thr	Leu	Gly	Arg	Leu	Val	Gln	Ser	Phe	Asp			
	450				455						460							
Leu	Leu	Pro	Pro	Pro	Gly	Met	Asp	Lys										
	465				470													

<210> 60
 <211> 408
 <212> PRT
 <213> Oryza sativa

<220>
 <221> PEPTIDE
 <222> (0)...(0)
 <223> line 1C-038-56 polypeptide sequence

Asp	Val	Gln	Gln	His	Ser	Gly	Ser	Ser	Ser	Ser	Ser	Thr	Glu	Ser	Asp
1				5				10						15	
Val	Gln	Glu	Thr	Ala	Ala	Val	Ala	Val	Ala	Asp	Pro	Ser	Pro	Arg	Ser
			20					25					30		
Glu	Val	Val	Asp	Gly	Glu	Ser	Pro	Pro	Gln	Pro	Gly	Gly	Glu	Ala	Ala
		35					40					45			
Ser	His	Gln	Gln	Gln	Gln	Lys	Glu	Met	Lys	Leu	Lys	Lys	Pro	Asp	Lys
	50					55					60				
Ile	Leu	Pro	Cys	Pro	Arg	Cys	Ser	Ser	Met	Asp	Thr	Lys	Phe	Cys	Tyr
	65				70					75					80
Phe	Asn	Asn	Tyr	Asn	Val	Asn	Gln	Pro	Arg	His	Phe	Cys	Lys	His	Cys
			85					90						95	
Gln	Arg	Tyr	Trp	Thr	Ala	Gly	Gly	Ala	Met	Arg	Asn	Val	Pro	Val	Gly

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Ala	Gly	Arg	100	Lys	Asn	Lys	Asn	105	Ala	Thr	Ala	Ala	Ala	110	His	Phe	Leu
His	Arg	115	Arg	Ala	Cys	Ala	Ala	120	Ala	Ala	Ala	Met	Pro	125	Ala	Ala	Pro
His	Asp	130	Ala	Thr	Asn	Ala	Thr	135	Val	Leu	Ser	Phe	Gly	140	Gly	Gly	Gly
145	Gly	His	Asp	Ala	Leu	Pro	Val	150	Thr	Leu	Asp	Leu	Ala	155	Asp	Lys	Met
160	Arg	Leu	Gly	165	Lys	Glu	Gly	Leu	Val	Ala	His	Ala	Arg	170	Asn	Ala	Asp
175	Ala	Ala	Ala	180	Cys	Ser	Glu	Val	Ser	185	Ser	Asn	Arg	190	Asp	Asp	Glu
195	Gly	Asn	Thr	Val	Ala	Lys	Pro	200	Ala	Asn	Gly	Leu	Gln	205	Gln	His	Pro
210	Pro	Pro	His	His	His	His	His	215	Ser	Ala	Met	Asn	Gly	220	Gly	Gly	Ile
225	Pro	Tyr	Tyr	Thr	Ser	Gly	Ile	230	Ala	Ile	Pro	Ile	Tyr	235	Pro	Ala	Ala
240	Ala	Tyr	Trp	Gly	245	Cys	Met	Ile	Pro	Pro	Pro	Gly	Ala	250	Trp	Ser	Leu
255	Trp	Pro	Ala	Thr	Val	Gln	Ser	Gln	260	Ala	Ile	Ser	Ser	265	Ser	Ser	Pro
270	Thr	Ser	Ala	Thr	Pro	Ser	Val	275	Ser	Ser	Phe	Thr	Leu	280	Gly	Lys	His
285	Arg	Glu	Gly	Gly	Asp	His	Glu	290	Ala	Arg	Asp	His	His	295	Gly	Asn	Gly
300	Val	Trp	Val	Pro	Lys	Thr	Ile	305	Arg	Ile	Asp	Asn	Ala	310	Asp	Glu	Val
315	Arg	Ser	Ser	Ile	Arg	Ser	Leu	320	Phe	Ala	Phe	Arg	Gly	325	Gly	Asp	Lys
330	Asp	Asp	Asn	Asp	Asp	Asp	Gly	335	Thr	Ser	Val	His	Lys	340	Leu	Ala	Thr
345	Thr	Val	Phe	Glu	Pro	Lys	Arg	350	Asp	Gly	Lys	Thr	Ala	355	Lys	His	Pro
360	Ile	Thr	Ser	Leu	Pro	Leu	Leu	365	His	Thr	Asn	Pro	Val	370	Ala	Leu	Thr
375	Ser	Ala	Thr	Phe	Gln	Glu	Gly	380	Ser					385			Arg
390																	400
405																	

<210> 61
 <211> 290
 <212> PRT
 <213> oryza sativa

<220>
 <221> PEPTIDE
 <222> (0)...(0)
 <223> line 1C-041-47 polypeptide sequence

<400> 61
 Met Gly Ile Lys Gly Leu Thr Lys Leu Leu Ala Asp Asn Ala Pro Lys
 1 5 10 15
 Ala Met Lys Glu Gln Lys Phe Glu Ser Tyr Phe Gly Arg Arg Ile Ala
 20 25 30
 Val Asp Ala Ser Met Ser Ile Tyr Gln Phe Leu Ser Phe Ala Arg Tyr
 35 40 45
 Ser Lys Arg Glu Asp Ala Thr Lys Glu Leu Thr Glu Ala Val Glu Glu
 50 55 60
 Gly Asp Lys Asp Ala Ile Glu Lys Phe Ser Lys Arg Thr Val Lys Val
 65 70 75 80
 Thr Lys Gln His Asn Glu Glu Cys Lys Arg Leu Leu Arg Leu Met Gly

20010-0405A.3123														
85					90					95				
Val	Pro	Val	Val	Glu	Val	Tyr	Ala	Val	Ala	Ser	Glu	Asp	Met	Asp
Leu	Thr	Phe	Gly	Ala	Pro	Arg	Phe	Leu	Arg	His	Leu	Met	Asp	Pro
Ser	Lys	Lys	Ile	Pro	Val	Met	Glu	Phe	Glu	Val	Ala	Lys	Val	Leu
Glu	Leu	Glu	Leu	Thr	Met	Asp	Gln	Phe	Ile	Asp	Leu	Cys	Ile	Leu
Gly	Cys	Asp	Tyr	Cys	Asp	Ser	Ile	Lys	Gly	Ile	Gly	Gly	Gln	Thr
Leu	Lys	Leu	Ile	Arg	Gln	His	Gly	Ser	Ile	Glu	Ser	Ile	Leu	Glu
Ile	Asn	Lys	Asp	Arg	Tyr	Gln	Ile	Pro	Glu	Asp	Trp	Pro	Tyr	Gln
Ala	Arg	Arg	Leu	Phe	Lys	Glu	Pro	Asn	Val	Thr	Leu	Asp	Ile	Pro
Leu	Lys	Trp	Asn	Ala	Pro	Asp	Glu	Glu	Ala	Ile	Glu	Lys	Ile	Lys
Ala	Lys	Asn	Lys	Ser	Ser	Gln	Gly	Arg	Leu	Glu	Ser	Phe	Phe	Lys
Val	Val	Ser	Thr	Ser	Val	Pro	Leu	Lys	Arg	Lys	Asp	Thr	Ser	Glu
Pro	Thr	Lys	Ala	Val	Ala	Asn	Lys	Lys	Thr	Lys	Gly	Ala	Gly	Gly
Lys	Lys													

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<210> 62
<211> 552
<212> PRT
<213> Oryza sativa
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<220>  
<221> PEPTIDE  
<222> (0)...(0)  
<223> line 1C-064-20 polypeptide sequence
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<400>	62														
Met	Ala	Ser	Ala	Pro	Gly	Asp	Gly	Lys	Gln	Gly	Gly	Gly	Gly	Gly	Gly
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Pro	Ala	Val	Gly	Ile	Asp	Leu	Gly	Thr	Thr	Tyr	Ser	Cys	Val	Ala	Val
			20					25					30		
Trp	Arg	His	Asp	Arg	Gly	Glu	Val	Ile	Ala	Asn	Asp	Gln	Arg	Asn	Arg
		35					40					45			
Leu	Thr	Pro	Ser	Cys	Val	Ala	Phe	Thr	Ala	Asp	Asp	Asp	Asp	Ser	Phe
	50					55					60				
Val	Gly	Asp	Ala	Ala	Phe	Asn	Gln	Ser	Ala	Leu	Asn	Pro	Thr	Asn	Thr
65					70					75				80	
Ile	Phe	Glu	Val	Lys	Arg	Leu	Ile	Gly	Arg	Arg	Phe	Ser	Asp	Asp	Ser
				85					90					95	
Val	Gln	Lys	Asp	Ile	Lys	Leu	Trp	Pro	Phe	Lys	Val	Val	Ala	Gly	Gln
			100					105					110		
Glu	Asp	Arg	Pro	Met	Ile	Val	Val	Arg	His	Glu	Gly	Glu	Glu	Arg	Gln
		115					120					125			
Phe	Met	Pro	Glu	Glu	Ile	Ser	Ser	Met	Val	Leu	Ala	Lys	Met	Arg	Glu
	130					135					140				
Thr	Ala	Glu	Val	Tyr	Leu	Gly	Lys	Thr	Val	Thr	Lys	Ala	Val	Ile	Thr
145					150					155				160	
Val	Pro	Val	Tyr	Phe	Asn	Asn	Ala	Gln	Arg	Gln	Ala	Thr	Met	Asp	Ala
				165					170					175	
Gly	Ala	Ile	Ala	Gly	Leu	Asn	Val	Met	Arg	Ile	Ile	Asn	Glu	Pro	Thr

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Ala	Ala	Ala	180	Leu	Ala	Tyr	Cys	Leu	185	Glu	Lys	Met	Pro	Val	190	Ser	Asn	Lys
Gly	Arg	Met	195	Val	Leu	Val	Phe	Asp	200	Leu	Gly	Gly	Gly	Thr	205	Phe	Asp	Ile
Ser	Leu	Leu	210	Asn	Ile	Asp	215	Pro	Gly	Glu	Gly	Thr	220	Ala	Gly	Asp	Thr	His
225	Leu	Gly	Gly	Ala	Asp	230	Phe	Asp	Asn	Glu	Leu	Val	Lys	His	Ser	Leu	Arg	240
Glu	Phe	Asn	Arg	Lys	His	Gly	Ser	Met	250	Asp	Ile	Glu	Ser	Asn	Gln	Lys		255
Ala	Leu	Arg	260	Arg	Leu	Arg	Thr	Ala	265	Cys	Glu	Arg	Ala	Lys	Arg	Met	Leu	270
Ser	Ser	Thr	275	Met	Gln	Thr	Thr	280	Ile	Glu	Val	Asp	Ser	Leu	His	Gln	Gly	285
Ile	Asp	Phe	Arg	Val	Thr	Leu	Thr	295	Arg	Ser	Arg	Phe	Glu	Glu	Leu	Asn		300
305	Lys	Asp	Leu	Phe	Ser	Lys	Cys	Met	Glu	Ala	Met	Glu	Asn	Cys	Leu	Arg		315
Asp	Ala	Lys	Val	Asp	Lys	Trp	Ser	Val	330	Asp	Asp	Val	Val	Leu	Val	Gly		335
Gly	Ser	Thr	340	Arg	Ile	Pro	Lys	Val	345	Gln	Lys	Met	Leu	Ser	Glu	Phe	Phe	350
Asp	Gly	Lys	Glu	Leu	Cys	Arg	Ser	Ile	360	Asn	Pro	Asp	Glu	Ala	Val	Ala		365
Tyr	Gly	Ala	Ala	Ile	Gln	Ala	Ser	Ile	375	Leu	Cys	Gly	Gly	Thr	Asp	Asp		380
385	Lys	Arg	Leu	Val	Asp	Met	Leu	Leu	395	Arg	Glu	Val	Thr	Pro	Leu	Ser	Leu	400
Gly	Val	Glu	Thr	Glu	Asp	Asn	Cys	Thr	410	Met	Ser	Val	Val	Ile	Pro	Arg		415
Asn	Thr	Ala	Ile	Pro	Thr	Lys	Lys	Val	425	Lys	Asn	Phe	Thr	Thr	Leu	Tyr		430
Asp	Asn	Gln	Ile	Asn	Val	Ser	Phe	Pro	440	Val	Tyr	Glu	Gly	Glu	Ser	Ala		445
Asn	Thr	Lys	Asp	Asn	Asn	Leu	Leu	Gly	455	Glu	Phe	Thr	Leu	Tyr	Gly	Ile		460
465	Pro	Pro	Ala	Pro	Lys	Arg	Val	Pro	470	Ser	Ile	Asp	Val	Thr	Phe	Asp	Ile	475
Asp	Ala	Asn	Gly	Val	Leu	Asn	Val	Ser	485	Ala	Glu	His	Lys	Val	Thr	Gly		490
Gln	Lys	Asn	Ser	Ile	Thr	Ile	Thr	Asn	500	Arg	Ser	Gly	Arg	Leu	Asn	Gln		505
Glu	Glu	Ile	Asp	Arg	Met	Ala	Leu	Glu	515	Pro	Glu	Arg	His	Lys	Met	Lys		520
Arg	Ile	Lys	Leu	His	Glu	Val	Val		535									540
545					550													

<210> 63

<211> 479

<212> PRT

<213> oryza sativa

<220>

<221> PEPTIDE

<222> (0)...(0)

<223> line 1C-109-35 polypeptide sequence

<400> 63

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Ser	Ala	Ser	Val	Ala	Asp	Trp	Leu	Asn	Lys	Gly	Asp	Asn	Ala	Trp	Gln

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20 25 30
 Leu Val Ala Thr Leu Val Gly Leu Gln Ser Val Pro Gly Leu Val
 35 40 45
 Val Leu Tyr Gly Gly Val Val Lys Lys Lys Trp Ala Val Asn Ser Ala
 50 55 60
 Phe Met Ala Leu Tyr Ala Phe Ala Ala Val Trp Ile Cys Trp Val Thr
 65 70 75 80
 Trp Ala Tyr Asn Met Ser Phe Gly Glu Lys Leu Leu Pro Ile Trp Gly
 85 90 95
 Lys Ala Arg Pro Ala Leu Asp Gln Gly Leu Leu Val Gly Arg Ala Ala
 100 105 110
 Leu Pro Ala Thr Val His Tyr Arg Ala Asp Gly Ser Val Glu Thr Ala
 115 120 125
 Ala Val Glu Pro Leu Tyr Pro Met Ala Thr Val Val Tyr Phe Gln Cys
 130 135 140
 Val Phe Ala Ala Ile Thr Leu Ile Leu Val Ala Gly Ser Leu Leu Gly
 145 150 155 160
 Arg Met Ser Phe Leu Ala Trp Met Ile Phe Val Pro Leu Trp Leu Thr
 165 170 175
 Phe Ser Tyr Thr Val Gly Ala Phe Ser Leu Trp Gly Gly Gly Phe Leu
 180 185 190
 Phe His Trp Gly Val Ile Asp Tyr Cys Gly Gly Tyr Val Ile His Val
 195 200 205
 Ser Ala Gly Ile Ala Gly Phe Thr Ala Ala Tyr Trp Val Gly Pro Arg
 210 215 220
 Ala Gln Lys Asp Arg Glu Arg Phe Pro Pro Asn Asn Ile Leu Phe Thr
 225 230 235 240
 Leu Thr Gly Ala Gly Leu Leu Trp Met Gly Trp Ala Gly Phe Asn Gly
 245 250 255
 Gly Gly Pro Tyr Ala Ala Asn Ser Val Ala Ser Met Ala Val Leu Asn
 260 265 270
 Thr Asn Ile Cys Thr Ala Met Ser Leu Ile Val Trp Thr Cys Leu Asp
 275 280 285
 Val Ile Phe Phe Lys Lys Pro Ser Val Val Gly Ala Val Gln Gly Met
 290 295 300
 Ile Thr Gly Leu Val Cys Ile Thr Pro Ala Ala Gly Val Val Gln Gly
 305 310 315 320
 Trp Ala Ala Leu Val Met Gly Val Leu Ala Gly Ser Ile Pro Trp Tyr
 325 330 335
 Thr Met Met Ile Leu His Lys Arg Ser Lys Ile Leu Gln Arg Val Asp
 340 345 350
 Asp Thr Leu Gly Val Phe His Thr His Gly Val Ala Gly Leu Leu Gly
 355 360 365
 Gly Leu Leu Thr Gly Leu Phe Ala Glu Pro Thr Leu Cys Asn Leu Phe
 370 375 380
 Leu Pro Val Ala Asp Ser Arg Gly Ala Phe Tyr Gly Gly Ala Gly Gly
 385 390 395 400
 Ala Gln Phe Gly Lys Gln Ile Ala Gly Gly Leu Phe Val Val Ala Trp
 405 410 415
 Asn Val Val Val Thr Ser Leu Ile Cys Leu Ala Ile Asn Leu Leu Val
 420 425 430
 Pro Leu Arg Met Pro Asp Asp Lys Leu Glu Val Gly Asp Asp Ala Val
 435 440 445
 His Gly Glu Glu Ala Tyr Ala Leu Trp Gly Asp Gly Glu Met Tyr Asp
 450 455 460
 Val Thr Lys His Gly Ser Asp Ala Ala Val Ala Pro Val Val Val
 465 470 475

<210> 64
 <211> 2177
 <212> PRT
 <213> Oryza sativa

<220>
 <221> PEPTIDE
 <222> (0)...(0)
 <223> line 1C-109-51 polypeptide sequence

<400> 64

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Tyr	Glu	Tyr	Arg	Ala	Asn	Ser	Ser	Leu	Val	Leu	Thr	Thr	Asp	Ser	Arg
			20					25					30		
Pro	Arg	Asp	Thr	His	Glu	Pro	Thr	Gly	Glu	Pro	Glu	Thr	Leu	Trp	Gly
		35					40					45			
Arg	Ile	Asp	Pro	Arg	Ser	Phe	Gly	Asp	Arg	Ala	Val	Gln	Ala	Lys	Pro
	50					55					60				
Pro	Glu	Leu	Glu	Glu	Lys	Leu	Thr	Lys	Ser	Arg	Lys	Lys	Lys	Ala	Ala
65					70					75					80
Ala	Ser	Asp	Pro	Asp	Asp	Leu	His	Arg	Arg	Asp	Ala	Lys	Arg	Arg	Arg
				85					90					95	
Arg	Ala	Ala	Ala	Ala	Gln	Ser	Glu	Val	Ser	Val	Leu	Ser	Leu	Thr	Asp
			100					105					110		
Asp	Val	Val	Tyr	Lys	Pro	Gln	Thr	Lys	Glu	Thr	Arg	Ala	Ala	Tyr	Glu
	115						120					125			
Ala	Leu	Leu	Ser	Val	Ile	Gln	Gln	Gln	Phe	Gly	Gly	Gln	Pro	Leu	Asp
	130					135					140				
Val	Leu	Gly	Gly	Ala	Ala	Asp	Glu	Val	Leu	Ala	Val	Leu	Lys	Asn	Asp
145					150					155					160
Lys	Ile	Lys	Ser	Pro	Asp	Lys	Lys	Lys	Glu	Ile	Glu	Lys	Leu	Leu	Asn
				165					170					175	
Pro	Ile	Ser	Asn	Gln	Met	Phe	Asp	Gln	Ile	Val	Ser	Ile	Gly	Lys	Leu
			180					185					190		
Ile	Thr	Asp	Phe	His	Asp	Ala	Ser	Ala	Gly	Asp	Ser	Ala	Ala	Ala	Pro
		195					200					205			
Ser	Gly	Asp	Gly	Met	Asp	Thr	Ala	Leu	Asp	Asp	Asp	Ile	Gly	Val	Ala
	210					215					220				
Val	Glu	Phe	Glu	Glu	Asn	Glu	Asp	Asp	Glu	Glu	Ser	Asp	Phe	Asp	Gln
	225				230					235					240
Val	Gln	Asp	Asp	Leu	Asp	Glu	Asp	Glu	Asp	Asp	Asp	Leu	Pro	Glu	Ser
				245					250					255	
Asn	Ala	Pro	Gly	Ala	Met	Gln	Met	Gly	Gly	Glu	Leu	Asp	Asp	Asp	Asp
			260					265					270		
Met	Gln	Asn	Ser	Asn	Glu	Gly	Leu	Thr	Ile	Asn	Val	Gln	Asp	Ile	Asp
		275					280					285			
Ala	Tyr	Trp	Leu	Gln	Arg	Lys	Val	Ser	Gln	Ala	Tyr	Glu	Asp	Ile	Asp
	290					295					300				
Pro	Gln	His	Ser	Gln	Lys	Leu	Ala	Glu	Glu	Ile	Leu	Lys	Ile	Ile	Ala
	305				310					315					320
Glu	Gly	Asp	Asp	Arg	Asp	Val	Glu	Asn	Arg	Leu	Val	Met	Leu	Leu	Asp
				325					330				335		
Tyr	Glu	Lys	Phe	Asp	Leu	Ile	Lys	Leu	Leu	Leu	Arg	Asn	Arg	Leu	Lys
			340					345					350		
Ile	Val	Trp	Cys	Thr	Arg	Leu	Ala	Arg	Ala	Glu	Asp	Gln	Glu	Gln	Arg
		355					360					365			
Lys	Lys	Ile	Glu	Glu	Asp	Met	Gly	Asn	Pro	Thr	Leu	Thr	Pro	Ile	
	370					375				380					
Leu	Glu	Gln	Leu	His	Ala	Thr	Arg	Ala	Ser	Ala	Lys	Glu	Arg	Gln	Lys
	385				390					395					400
Asn	Leu	Glu	Lys	Ser	Ile	Arg	Asp	Glu	Ala	Lys	Arg	Leu	Thr	Lys	Ser
				405					410					415	
Glu	Asn	Thr	Gly	Ile	Asp	Gly	Ala	Arg	Asp	Arg	Arg	Ala	Val	Asp	Arg
			420					425					430		
Asp	Met	Glu	Ser	Gly	Trp	Leu	Lys	Gly	Gln	Arg	Gln	Leu	Leu	Asp	Leu
		435					440					445			

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Asp	Ser	Leu	Ser	Phe	His	Gln	Gly	Gly	Leu	Leu	Met	Ala	Asn	Lys	Lys
450						455					460				
Cys	Glu	Leu	Pro	Pro	Gly	Ser	Phe	Arg	Thr	Pro	His	Lys	Gly	Tyr	Glu
465					470					475					480
Glu	Val	His	Val	Pro	Ala	Leu	Lys	Ala	Lys	Pro	Tyr	Glu	Thr	Gly	Glu
				485					490					495	
Lys	Ile	Val	Lys	Ile	Ser	Asp	Met	Pro	Glu	Trp	Ala	Gln	Pro	Ala	Phe
			500					505					510		
Ala	Lys	Met	Thr	Gln	Leu	Asn	Arg	Val	Gln	Ser	Lys	Val	Tyr	Glu	Thr
		515					520					525			
Ala	Leu	Phe	Lys	Pro	Asp	Asn	Ile	Leu	Leu	Cys	Ala	Pro	Thr	Gly	Ala
	530					535					540				
Gly	Lys	Thr	Asn	Val	Ala	Val	Leu	Thr	Ile	Leu	Gln	Gln	Ile	Gly	Leu
545					550					555					560
His	Met	Lys	Asp	Gly	Val	Phe	Asp	Asn	Thr	Lys	Tyr	Lys	Ile	Val	Tyr
				565					570					575	
Val	Ala	Pro	Met	Lys	Ala	Leu	Val	Ala	Glu	Val	Val	Gly	Asn	Leu	Ser
			580					585					590		
Ala	Arg	Leu	Ser	Ala	Tyr	Gly	Ile	Thr	Val	Arg	Glu	Leu	Ser	Gly	Asp
		595					600					605			
Gln	Asn	Leu	Thr	Lys	Gln	Gln	Ile	Asp	Glu	Thr	Gln	Ile	Ile	Val	Thr
	610				615						620				
Thr	Pro	Glu	Lys	Trp	Asp	Ile	Val	Thr	Arg	Lys	Ser	Gly	Asp	Arg	Thr
625					630					635					640
Tyr	Thr	Gln	Met	Val	Lys	Leu	Leu	Ile	Ile	Asp	Glu	Ile	His	Leu	Leu
				645					650					655	
His	Asp	Asn	Arg	Gly	Pro	Val	Leu	Glu	Ser	Ile	Val	Ser	Arg	Thr	Val
			660					665					670		
Arg	Gln	Ile	Glu	Thr	Thr	Lys	Glu	His	Ile	Arg	Leu	Val	Gly	Leu	Ser
		675					680					685			
Ala	Thr	Leu	Pro	Asn	Tyr	Glu	Asp	Val	Ala	Val	Phe	Leu	Arg	Val	Arg
	690					695					700				
Ser	Asp	Gly	Leu	Phe	His	Phe	Asp	Asn	Ser	Tyr	Arg	Pro	Cys	Pro	Leu
705					710					715					720
Ala	Gln	Gln	Tyr	Ile	Gly	Ile	Thr	Val	Arg	Lys	Pro	Leu	Gln	Arg	Phe
				725					730					735	
Gln	Leu	Met	Asn	Glu	Ile	Cys	Tyr	Glu	Lys	Val	Met	Ala	Ser	Ala	Gly
			740					745					750		
Lys	His	Gln	Val	Leu	Ile	Phe	Val	His	Ser	Arg	Lys	Glu	Thr	Ala	Lys
		755					760					765			
Thr	Ala	Arg	Ala	Ile	Arg	Asp	Thr	Ala	Leu	Ala	Asn	Asp	Thr	Leu	Asn
	770					775					780				
Arg	Phe	Leu	Lys	Asp	Asp	Ser	Ala	Ser	Gln	Glu	Ile	Leu	Gly	Ser	Gln
785					790					795					800
Ala	Glu	Leu	Val	Lys	Ser	Ser	Asp	Leu	Lys	Asp	Leu	Leu	Pro	Tyr	Gly
				805					810					815	
Phe	Ala	Ile	His	His	Ala	Gly	Leu	Ala	Arg	Val	Asp	Arg	Glu	Leu	Val
			820					825					830		
Glu	Glu	Leu	Phe	Ala	Asp	Lys	His	Ile	Gln	Val	Leu	Val	Ser	Thr	Ala
		835					840					845			
Thr	Leu	Ala	Trp	Gly	Val	Asn	Leu	Pro	Ala	His	Thr	Val	Ile	Ile	Lys
	850					855					860				
Gly	Thr	Gln	Ile	Tyr	Asn	Pro	Glu	Lys	Gly	Ala	Trp	Thr	Glu	Leu	Ser
865					870					875					880
Pro	Leu	Asp	Val	Met	Gln	Met	Leu	Gly	Arg	Ala	Gly	Arg	Pro	Gln	Tyr
				885					890					895	
Asp	Thr	His	Gly	Glu	Gly	Ile	Ile	Leu	Thr	Gly	His	Ser	Glu	Leu	Gln
			900					905					910		
Tyr	Tyr	Leu	Ser	Leu	Met	Asn	Gln	Gln	Leu	Pro	Ile	Glu	Ser	Gln	Phe
			915				920					925			
Ile	Ser	Arg	Leu	Ala	Asp	Gln	Leu	Asn	Ala	Glu	Ile	Val	Leu	Gly	Thr
	930					935					940				
Ile	Gln	Asn	Ala	Arg	Glu	Ala	Cys	Ser	Trp	Leu	Gly	Tyr	Thr	Tyr	Leu

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945 Tyr Ile Arg Met Leu 950 Arg Asn Pro Thr Leu 955 Tyr Gly Leu Pro Ala 960 Asp
 Ile Met Glu Thr 965 Asp Lys Thr Leu Asp 970 Glu Arg Arg Ala Asp 975 Leu Val
 His Ser Ala Ala Asn Leu Leu Asp 985 Arg Asn Asn Leu Ile Lys Tyr Asp
 Arg Lys Thr Gly Tyr Phe 1000 Val Thr Asp Leu Gly Arg Ile Ala Ser
 Tyr Tyr Tyr Ile Ser His Gly Thr Ile Ser Thr Tyr Asn Glu Tyr Leu
 1025 Lys Pro Thr Met Gly Asp Ile Glu Leu Cys Arg Leu Phe Ser Leu Ser
 Glu Glu Phe Lys Tyr Val Ser Val Arg Gln Asp Glu Lys Met Glu Leu
 Ala Lys Leu Leu Asp Arg Val Pro Ile Pro Val Lys Glu Ser Leu Glu
 Glu Pro Ser Ala Lys Ile Asn Val Leu Leu Gln Ala Tyr Ile Ser Arg
 Leu Lys Leu Glu Gly Leu Ser Leu Ser Ser Asp Met Val Tyr Ile Arg
 1105 Gln Ser Ala Gly Arg Leu Leu Arg Ala Leu Phe Glu Ile Val Leu Lys
 Arg Gly Trp Ala Gln Leu Ala Glu Lys Ala Leu Asn Leu Cys Lys Met
 Ile Asp Lys Gln Met Trp Asn Val Gln Thr Pro Leu Arg Gln Phe Pro
 Gly Ile Pro Lys Glu Ile Leu Met Lys Leu Glu Lys Lys Glu Leu Ala
 Trp Glu Arg Tyr Tyr Asp Leu Ser Ser Gln Glu Ile Gly Glu Leu Ile
 1185 Arg Phe Pro Lys Met Gly Arg Gln Leu His Lys Cys Ile His Gln Leu
 Pro Lys Leu Asn Leu Ser Ala His Val Gln Pro Ile Thr Arg Thr Val
 Leu Gly Phe Glu Leu Thr Ile Thr Pro Asp Phe Gln Trp Asp Asp Lys
 Val His Gly Tyr Val Glu Pro Phe Trp Val Ile Val Glu Asp Asn Asp
 Gly Glu Asn Ile Leu His His Glu Tyr Phe Met Val Lys Lys Gln Tyr
 1265 Val Asp Glu Asp His Thr Leu Asn Phe Thr Val Pro Ile Tyr Glu Pro
 Leu Pro Pro Gln Tyr Phe Ile Arg Val Val Ser Asp Lys Trp Leu Gly
 Ser Gln Thr Ile Leu Pro Val Cys Phe Arg His Leu Ile Leu Pro Glu
 Lys Tyr Ala Pro Pro Thr Glu Leu Leu Asp Leu Gln Pro Leu Pro Val
 Thr Ala Leu Arg Asn Ala Arg Tyr Glu Gly Leu Tyr Ser Ala Phe Lys
 1345 His Phe Asn Pro Ile Gln Thr Gln Val Phe Thr Val Leu Tyr Asn Thr
 Asp Asp Ser Val Leu Val Ala Ala Pro Thr Gly Ser Gly Lys Thr Ile
 Cys Ala Glu Phe Ala Ile Leu Arg Asn His Gln Lys Ala Val Ser Gly
 Glu Ser Asn Met Arg Val Val Tyr Ile Ala Pro Ile Glu Ala Leu Ala
 Lys Glu Arg Tyr Arg Asp Trp Glu Gln Lys Phe Gly Glu Phe Ala Arg
 1425 Val Val Glu Leu Thr Gly Glu Thr Ala Ala Asp Leu Lys Leu Leu Asp
 1445 1450 1455

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Lys Gly Glu Ile Ile Ile Ser Thr Pro Glu Lys Trp Asp Ala Leu Ser
 1460 1465 1470
 Arg Arg Trp Lys Gln Arg Lys Gln Val Gln Val Ser Leu Phe Ile
 1475 1480 1485
 Val Asp Glu Leu His Leu Ile Gly Ser Glu Lys Gly His Val Leu Glu
 1490 1495 1500
 Val Ile Val Ser Arg Met Arg Arg Ile Ala Ser His Ile Gly Ser Asn
 1505 1510 1515 1520
 Ile Arg Ile Val Ala Leu Ser Ala Ser Leu Ala Asn Ala Lys Asp Leu
 1525 1530 1535
 Gly Glu Trp Ile Gly Ala Thr Ser His Gly Leu Phe Asn Phe Pro Pro
 1540 1545 1550
 Ala Val Arg Pro Val Pro Leu Glu Ile His Ile Gln Gly Val Asp Ile
 1555 1560 1565
 Ala Asn Phe Glu Ala Arg Met Gln Ala Met Thr Lys Pro Thr Tyr Thr
 1570 1575 1580
 Ala Ile Thr Gln His Ala Lys Asn Gly Lys Pro Ala Leu Val Phe Val
 1585 1590 1595 1600
 Pro Thr Arg Lys His Ala Arg Leu Thr Ala Leu Asp Leu Cys Ala Tyr
 1605 1610 1615
 Ser Ser Ala Glu Gly Gly Gly Thr Pro Phe Leu Leu Gly Ser Glu Asp
 1620 1625 1630
 Glu Met Asp Ala Phe Thr Gly Gly Ile Ser Asp Glu Thr Leu Lys Tyr
 1635 1640 1645
 Thr Leu Lys Cys Gly Val Gly Tyr Leu His Glu Gly Leu Ser Asp Leu
 1650 1655 1660
 Glu Gln Glu Val Val Thr Gln Leu Phe Leu Ser Gly Arg Ile Gln Val
 1665 1670 1675 1680
 Cys Val Ala Ser Ser Thr Val Cys Trp Gly Arg Ser Leu Pro Ala His
 1685 1690 1695
 Leu Val Val Val Met Gly Thr Gln Tyr Asp Gly Arg Glu Asn Ala
 1700 1705 1710
 His Thr Asp Tyr Pro Ile Thr Asp Leu Leu Gln Met Met Gly His Ala
 1715 1720 1725
 Ser Arg Pro Leu Gln Asp Asn Ser Gly Lys Cys Val Ile Leu Cys His
 1730 1735 1740
 Ala Pro Arg Lys Glu Tyr Tyr Lys Lys Phe Leu Phe Glu Ala Phe Pro
 1745 1750 1755 1760
 Val Glu Ser His Leu His His Phe Leu His Asp His Met Asn Ala Glu
 1765 1770 1775
 Val Val Val Gly Val Ile Glu Asn Lys Gln Asp Ala Val Asp Tyr Leu
 1780 1785 1790
 Thr Trp Thr Phe Met Tyr Arg Arg Leu Thr Lys Asn Pro Asn Tyr Tyr
 1795 1800 1805
 Asn Leu Gln Gly Val Ser His Arg His Leu Ser Asp His Leu Ser Glu
 1810 1815 1820
 Leu Val Glu Thr Val Leu Asn Asp Leu Glu Ser Ser Lys Cys Val Ala
 1825 1830 1835 1840
 Ile Glu Glu Asp Met Tyr Leu Lys Pro Leu Asn Leu Gly Leu Ile Ala
 1845 1850 1855
 Ser Tyr Tyr Tyr Ile Ser Tyr Thr Thr Ile Glu Arg Phe Ser Ser Met
 1860 1865 1870
 Leu Thr Gln Lys Thr Lys Met Lys Gly Leu Leu Glu Ile Leu Ala Ser
 1875 1880 1885
 Ala Ser Glu Tyr Ala Glu Leu Pro Ser Arg Pro Gly Glu Glu Asp Phe
 1890 1895 1900
 Ile Glu Lys Leu Val Arg His Gln Arg Phe Ser Ile Glu Lys Pro Arg
 1905 1910 1915 1920
 Tyr Gly Asp Pro His Val Lys Ala Asn Ala Leu Leu Gln Ala His Phe
 1925 1930 1935
 Ser Arg His Thr Ile Leu Gly Asn Leu Ala Ala Asp Gln Arg Glu Ile
 1940 1945 1950
 Leu Leu Ser Ala His Arg Leu Leu Gln Ala Met Val Asp Val Ile Ser

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1955 1960 1965
 Ser Asn Gly Trp Leu Thr Leu Ala Leu Asn Ala Met Glu Leu Ser Gln
 1970 1975 1980
 Met Val Thr Gln Gly Met Trp Asp Arg Asp Ser Val Leu Leu Gln Leu
 1985 1990 1995 2000
 Pro His Phe Thr Lys Glu Leu Ala Arg Arg Cys Gln Glu Asn Glu Gly
 2005 2010 2015
 Arg Pro Ile Glu Ser Ile Phe Asp Leu Ala Glu Met Ser Ile Asp Glu
 2020 2025 2030
 Met Arg Asp Leu Leu Gln Gln Ser Asn Pro Gln Leu Gln Asp Ile Ile
 2035 2040 2045
 Glu Phe Phe Lys Arg Phe Pro Asn Val Asp Met Ala Tyr Glu Val Arg
 2050 2055 2060
 Glu Gly Asp Asp Ile Arg Ala Gly Asp Asn Val Thr Val Gln Val Thr
 2065 2070 2075 2080
 Leu Glu Arg Asp Met Thr Asn Leu Pro Ser Glu Val Gly Pro Val His
 2085 2090 2095
 Ala Pro Arg Tyr Pro Lys Pro Lys Glu Glu Gly Trp Trp Leu Val Ile
 2100 2105 2110
 Gly Asp Ser Thr Asn Gln Leu Leu Ala Ile Lys Arg Val Ala Leu
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 Gln Lys Arg Ala Arg Val Lys Leu Glu Phe Thr Ala Ala Ser Glu Ala
 2130 2135 2140
 Gly Arg Lys Glu Tyr Met Ile Tyr Leu Met Ser Asp Ser Tyr Leu Gly
 2145 2150 2155 2160
 Cys Asp Gln Glu Tyr Glu Phe Thr Val Asp Val Met Asp Ala Gly Gly
 2165 2170 2175
 Asp

<210> 65
 <211> 181
 <212> PRT
 <213> Oryza sativa

<220>
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 <222> (0)...(0)
 <223> line 1C-056-07 polypeptide sequence

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 35 40 45
 Gly Gly Gly Val Val Thr Trp Phe Tyr Thr His Asp Ser Ile Ala Ser
 50 55 60
 Ala Leu Val Ile Ile Ile Gly Ser Gly Val Leu Ala Phe Cys Leu Asn
 65 70 75 80
 Phe Ser Ile Phe Tyr Val Ile His Ser Thr Thr Ala Val Thr Phe Asn
 85 90 95
 Val Ala Gly Asn Leu Lys Val Ala Val Ala Val Leu Val Ser Trp Leu
 100 105 110
 Ile Phe Arg Asn Pro Ile Ser Pro Met Asn Ala Ile Gly Cys Ala Ile
 115 120 125
 Thr Leu Val Gly Cys Thr Phe Tyr Gly Tyr Val Arg His Leu Ile Ser
 130 135 140
 Gln Gln Gln Ala Val Ala Pro Gly Thr Gly Ser Pro Thr Thr Ser Gln
 145 150 155 160
 Thr Asn Ser Pro Arg Ser Arg Met Glu Met Leu Pro Leu Val Gly Asp

Lys Gln Glu Lys Val
180

<210> 66
<211> 793
<212> PRT
<213> Oryza sativa

<220>
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<223> line 1C-100-32 polypeptide sequence

<400> 66
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Ser Ser Ser Ala Val Leu Ala Ala Ala Asn Asn Thr Gly Gly Ala Gln
35 40 45
His Pro Met Trp Lys Thr Ser Leu Cys Ser Phe Phe Arg Arg Arg Ala
50 55 60
Ala Ser Ser Ala Asp Gly Cys Ser His Gly Asp Ser Cys Arg Tyr Ala
65 70 75 80
His ser Glu Glu Glu Leu Arg Pro Arg Pro Asp Gly Thr Trp Asp Pro
85 90 95
Thr Ser Asp Arg Ala Lys Lys Leu Arg Lys Val Ala Ala Asp Glu Val
100 105 110
Glu Glu Glu Val Val Thr Ile Asp Asp Lys Ala Leu Asp Lys Cys Leu
115 120 125
Val Gly Leu Pro Arg Gly Trp Ala Asn Asp Arg Leu Lys Thr Phe Leu
130 135 140
Gln Asp Lys Ala Arg Thr Asn Tyr Ser Ser Ile Leu Pro Pro Ala Leu
145 150 155 160
Leu Leu Gly Ile Ser Tyr Ala Thr Ala Lys Lys Lys Gly Met Thr
165 170 175
Val Gly Phe Val Thr Phe Glu Asn Ile Glu Gln Leu Lys Asn Ala Ile
180 185 190
Glu Val Leu Thr Glu Asn Gln Ser Gly Gly Lys Glu Ile Lys Ile Ala
195 200 205
Asp Ala Asn Arg Arg Ser His Gln Lys Leu His Thr Glu Lys Pro Val
210 215 220
Ser Asp Asn Gly Val Thr Thr Glu Asn Gly Thr Ser Val Asp Val Pro
225 230 235 240
Pro Gly Glu Thr Ser Ala Pro Glu Ala Ala Ile Ser Asn Lys Lys Ser
245 250 255
Val Arg Asp Ala Val Thr Pro Leu Ala His Met Ser Tyr Asn Asp Gln
260 265 270
Leu Glu His Lys Asn Asn Ser Val Ala Gln Ile Leu Lys Arg Leu Thr
275 280 285
Arg Asn Ala Arg Lys Ala Cys Pro Thr Gly Ile Pro Leu Pro Asp Trp
290 295 300
Val Phe Lys Ser Lys Glu Ile Gly Gly Leu Pro Cys Lys Leu Glu Gly
305 310 315 320
Ile Leu Glu Ser Pro Val Ile Asn Gly Tyr Arg Asn Lys Cys Glu Phe
325 330 335
Ser Val Gly Phe Ser Leu Glu Gly Lys Thr Val Gly Phe Met Leu
340 345 350
Gly Asn Phe Ser Thr Asp Met Ile Asp Lys Thr Lys Ser Arg Glu Gly
355 360 365
Val Thr Ala Val Glu Glu Pro Val Asp Cys Pro Asn Val Ser Glu Ile

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Ser 385	Cys	Lys	Tyr	Ala	Leu 390	Met	Phe	Gln	Asp	Phe 395	Leu	Gln	Ser	Ser	Ser	400
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Thr	Val	Arg	Glu 420	Gly	Arg	Cys	Arg	Ala 425	Gln	Ala	Val	Ala	Gln 430	Asn	Ala	
Glu	Thr	Gln 435	Ile	Ser	Glu	Val	Met 440	Leu	Ile	Val	Gln	Val 445	Cys	Ser	Thr	
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Ala 465	Leu	Gln	Gln	Gly	Ala 470	Ala	Thr	Cys	Ser	Pro 475	Pro	Leu	Pro	Leu	Thr 480	
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Ala	Val	Ser 595	Asp	Ala	Glu	Arg	Asn 600	Ala	Leu	Ile	Asn	Gly 605	Val	Ser	Asn	
Cys	Arg 610	Phe	Val	Cys	Gly	Lys 615	Ala	Glu	Asp	Val	Met 620	Gly	Ser	Leu	Leu	
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Lys	Ser	Gln 675	Gln	Leu	Gly	Asp	Ala 680	Pro	Ala	Asp	Ser	Ser 685	Ser	Ser	Ala	
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Cys	Leu	Glu	Asp 740	Arg	Lys	Thr	Ser	Asp 745	Asp	Gly	Ser	Ser	Ile 750	Ser	Asn	
Asn	Asp	Val 755	Thr	Ala	Ala	Thr	Ala 760	Cys	Gln	Phe	Glu	Asp 765	Ile	Val	Ala	
Ile	Val 770	Asp	Pro	Pro	Arg	Val 775	Gly	Leu	His	Pro	Thr 780	Val	Asn	Pro	Lys	
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<210> 67
<211> 143
<212> PRT
<213> Oryza sativa
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<221> PEPTIDE
<222> (0)...(0)
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<223> line 1C-142-27 polypeptide sequence

<400> 67

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      35      40      45
Lys Val Gly Gly Pro Gly Glu Gly Tyr Glu Glu Leu Val Ala Ala Leu
      50      55      60
Pro Thr Asp Asp Cys Arg Tyr Ala Val Phe Asp Phe Asp Phe Val Thr
65      70      75      80
Val Asp Asn Cys Gln Lys Ser Lys Ile Phe Phe Ile Ala Trp Ser Pro
      85      90      95
Thr Ala Ser Arg Ile Arg Ala Lys Ile Leu Tyr Ala Thr Ser Lys Gln
      100      105      110
Gly Leu Arg Arg Val Leu Asp Gly Val His Tyr Glu Val Gln Ala Thr
      115      120      125
Asp Ser Ser Glu Met Gly Tyr Asp Val Ile Arg Gly Arg Ala Gln
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<210> 68

<211> 452

<212> PRT

<213> Oryza sativa

<220>

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<222> (0)...(0)

<223> line 1C-140-04 polypeptide sequence

<400> 68

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Arg His Asp Phe Pro Glu Gly Phe Val Phe Gly Ala Gly Ser Ser Ala
      35      40      45
Phe Gln Val Glu Gly Ala Ala Ala Glu Asp Gly Arg Lys Pro Ser Ile
      50      55      60
Trp Asp Thr Phe Ile His Gln Gly Tyr Met Pro Asp Gly Ser Asn Ala
65      70      75      80
Asp Val Ser Ala Asp Gln Tyr His His Tyr Lys Glu Asp Val Lys Leu
      85      90      95
Met Tyr Asp Met Gly Leu Asp Ala Tyr Arg Phe Ser Ile Ala Trp Pro
      100      105      110
Arg Leu Ile Pro Asp Gly Arg Gly Glu Ile Asn Pro Lys Gly Leu Glu
      115      120      125
Tyr Tyr Asn Asn Leu Ile Asp Glu Leu Ile Met His Gly Ile Gln Pro
      130      135      140
His Val Thr Ile Tyr His Phe Asp Leu Pro Gln Ala Leu Gln Asp Glu
145      150      155      160
Tyr Gly Gly Ile Leu Ser Pro Arg Phe Ile Glu Asp Tyr Ser Ala Tyr
      165      170      175
Ala Glu Val Cys Phe Lys Asn Phe Gly Asp Arg Val Lys His Trp Ala
      180      185      190
Thr Phe Asn Gln Pro Asn Ile Glu Pro Ile Gly Gly Phe Asp Ala Gly
      195      200      205
Asp Arg Pro Pro Arg Arg Cys Ser Tyr Pro Phe Gly Thr Asn Cys Thr
210      215      220
Gly Gly Asp Ser Ser Thr Glu Pro Tyr Ile Val Ala His His Leu Leu

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225 230 235 240
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 Ala Ile Gln Gly Gln Ile Gly Ile Thr Leu Met Val Arg Trp His
 260 265 270
 Glu Pro Tyr Thr Asp Lys Thr Ala Asp Ala Ala Ala Ile Arg Met
 275 280 285
 Asn Glu Phe His Ile Gly Trp Phe Leu His Pro Leu Val His Gly Asp
 290 295 300
 Tyr Pro Pro Val Met Arg Ser Arg Val Gly Gly Arg Leu Pro Ser Ile
 305 310 315 320
 Thr Ala Ser Asp Ser Glu Lys Ile Arg Gly Ser Phe Asp Phe Ile Gly
 325 330 335
 Ile Asn His Tyr Tyr Val Ile Phe Val Gln Ser Ile Asp Ala Asn Glu
 340 345 350
 Gln Lys Leu Arg Asp Tyr Tyr Ile Asp Ala Gly Val Gln Gly Glu Asp
 355 360 365
 Asp Lys Glu Asn Ile Gln Cys His Ser Trp Ser Leu Gly Lys Val Leu
 370 375 380
 Asn His Leu Lys Leu Glu Tyr Gly Asn Pro Pro Val Met Ile His Glu
 385 390 395
 Met Val Ile Gln Ile His Arg Ile Ser Ser Glu Arg Ser Thr Thr Thr
 405 410 415
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<210> 69

<211> 6282

<212> DNA

<213> Artificial Sequence

<220>

<221> misc_feature

<222> (0)...(0)

<223> T-DNA sequence

artificial sequence

synthetic nucleic acid

<223> synthetic nucleic acid

<400> 69

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<213> Artificial Sequence

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